Human parat

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CQ831233 Sequence
AX280939 Sequence
AX428093 Sequence
BD266836 PTH funct
AF167095 Canis fam
U18315 Sus scrofa
AX328401 Cervus el
M74445 Opossum par
11776 Sequence
AX328401 Cervus el
BD24970 PTHIR and
AR302320 Sequence
AX32320 Sequence
AX32448 Sequence
AX122084 Danio rer
CQ831243 Sequence
AX42448 Sequence
AX132082 Danio rer
AB012944 Rattus no
AC098311 Rattus no
AC114361 Rattus no
AC114361 Rattus no
L31394 Rat parathy
AF132085 Danio rer
AR182685 Danio rer
AY132085 Danio rer
AR182689 Sequence
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PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS JR PC C12N15/09, C07K14/72, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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(bases 1 to 1320)
Gardella,T.J., Kronenberg,H.M. and Jr,J.T.P.
PHT receptor and screening assay utilizing the same.
Patent: JP 2002534081-A 1 15-OCT-2002;
THE GENERAL HOSPITAL CORP
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Description of Artificial Sequence: CDNA
Key Location/Qualifiers
CDS Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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AC098311
AC114361
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15-OCT-2002
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L19475 Rat parathy
M77184 Rat parathy
BC051981 MMS muscu
BC01346 Mus muscu
X78936 M.musculus
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BD266837 PTH funct
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AR270690 Sequence
AX548943 Sequence
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CQ714121 Sequence
I17767 Sequence 4
X68596 H.sapiens m
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BD266846 PTH funct
BD266847 PTH funct
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BD266835 PTH funct
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           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1241.6 1158.4 1155.2 1153.6 1011.2 983.8 977.8

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A61P19/10,
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1141 GCCAAGCCAGGGGTTCCAGCCACTGAGACTGAAACCCTACCAGTCACTATGGCGGTTCCC 1200
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                                                                                                                                                                                                                                                        other sequences; artificial sequences.

1 (bases 1 to 1335)
Cardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
FTH functional domain conjugate peptides, derivatives thereof sovel tethered ligand-receptor molecules
FALENTE, JP 2002533115-A 4 08-OCT-2002;
THE GENERAL HOSPITAL CORP
OS Artificial Sequence

PN JP 2002533115-A/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGA CGATGCATTAA CGCTCCTGCTCAGGCCTGGATGAGGAGGCCTCCGGGTCT
                                    1201 AAGGACGATGGATTCCTTAACGGCTCCTGCTCAGGCCTGGATGAGGAGGCCTCCGGGTCT
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Description of Artificial Sequence: modified PTH receptor CC
                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1999 JP 2000591171
31-DEC-1998 US 60/114577
THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
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larity 97.7%; Pred. No. 1.3e-253;
Conservative 0; Mismatches 4;
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Location/Qualifiers
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BD266835.1 GI:33076603
JP 2002533115-A/4.
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                                                                                                                                         Unclassified.

1 (bases 1 to 2051)
Segre, G.V., Kronenberg, H.M., Abou-Samra, A.-B., Juppner, H.,
Potts, J.T. Jr. and Schipani, E.
DNA and vectors encoding the parathyroid hormone receptor,
transformed cells, and recombinant production of PTHR proteins
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Pred. No. 3.6e-249;
0; Mismatches 3;
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Patent: US 5494806-A 3 27-FEB-1996;
Location/Qualifiers
1. 2051
/organism="unknown"
/mol_type="unassigned DNA"
                                                   2051 bp
US 5494806
                                                                3 from patent
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                                                                                         GI:1598121
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Matches 1245; Conservative
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/product="parathyroid hormone/parathyroid hormone
related-peptide receptor"
                                               hormone
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Pred. No. 7.8e-249;
0; Mismatches 4; Indels 0;
                                        /product="parathyroid hormone/parathyroid related-peptide receptor" /protein_id="AAA68098.1"
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                                                                            /protein_id="AAA6803
/db_xref="GI:467317
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llarity 99.7%;
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Rat parathyroid hormone/parathyroid hormone related-peptide
receptor mRNA, complete cds.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                L19475
L19975.1 GI:467316
parathyroid hormone; parathyroid hormone receptor; parathyroid
hormone-related protein; parathyroid hormone-related receptor.
Rattus norvegicus (Norway rat)
                  CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTGGTGTCCAC
                                                                                   GCTCCAGCCACTGAGACTGAAACCCTACCAGTCACTATGGCGGTTCCCAAGGACGATGGA
 CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTGGTGTACCAC
                                                                TACACCGTCTTCATGGCCTTGCCGTACACCGAGGTCTCAGGGACATTGTGGCAGATCCAG
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Levan, G., Szpirer, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Losses 1 to 1836)
Pausova, Z., Bourdon, J., Clayton, D., Mattei, M.G., Seldin, M.F., Janicic, N., Riviere, M., Szpirer, J., Levan, G., Szpirer, C., Goltzman, D. and Hendy, G.N.
Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHR) cDNA from a rat osteosarcoma (IMR 106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA.
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1. 1836
/organism="Rattus norvegicus"
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/db_xref="taxon:10116"
/cell_line="UMR 106"
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Genomics 20 (1), 20-26 (1994)
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PERATURES Location/Qualifiers 12065 / Organism="Rattus norvegicus" / Mol type="MankA" / Mol type="MankA" / Ab zref="taxon:10116" / Cell line="osteosarcoma" / Cell line="osteosarcoma" / Cool	Query Match 94.1%; Score 1241.6; DB 10; Length 2065; Best Local Similarity 99.7%; Pred. No. 7.7e-249; A indels 0; Gaps 0; Matches 1244; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Qy 13 TCCTCAGGGTATTTGACGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCC 672 672 672 Qy 133 TCCCTCACGTGGCTGTGCTCATCCTCGCCTATTTTAGGCGGCTGCACTGCACGCGCAAC 192 192 Db 673 TCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCGCAAC 132 Db 673 TCCCTCACGGTGGCTGTGCTATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCGCAAC 132	193 TACATCCACATGCACATGTTCTTATAGCTGCGCGCGCGACATCTTCGTGAAG 192
	Oy 1153 GCTCCAGCCACTGAGACTGAAACCCTACCAGTCACTATGGCGGTTCCCAAGGACGATGGA 1212	RESULT 5 RATPATHYR RATPATHYR LOCUGUS RATPATHYR LOCUGUS RATPATHYR LOCUGUS RATPATHYR RATPATHYR LOCUGUS RATE parathyroid hormone receptor mRNA, complete cds. M77184.1 G1:206034 W77184.1 G1:206034 RATUS morvedicus RATUS manualia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; RATUS MADU-Samra,AB. B., Jueppner,H., Force,T., Freeman,M.W., ROUG,XF., Schipani,B., Urena,P., Richards,J., Bonventre,J.V., ROUG,XF., Schipani,B., Urena,P., Richards,J., Bonventre,J.V., ROTERS,J. Kronenberg,H.M. and Segre'G,J. TITLE REFERENCE SAMP and inositol trisphosphates and increases intracellular free complete title: REDING PROC. Natl. Acad. Sci. U.S.A. 89 (7), 2732-2736 (1992) PUBMED Original source text: Rattus norvegicus CDNA to mRNA. COMPLET COMPLET COMPLET COMPLET COMPLET COMPLET COMPLET COMPLET REPRESEDENCE COMPLET COMP

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/ product = "bearathyroid hormone receptor 1"
/protein id="AAH51981.1"
/db_xref="Mid="AAH51981.1"
/db_xref="Mid="10354699"
/db_xref="Mid=197801"
/db_xref=
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Dr. Jim Lin, University of Iowa
Tissue procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: W. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAGRCDTROQYRKLLRSTLVLVPLFGVHYTVFMALPYTEVSGTLWOIOMHYEMLFNSF
OGETVALIVCPCNGEYOAEIRKSWSRWTLALDFKRKARSGSSSYSYGPWYSHTSYTNV
GPRAGISLPLSPRLLPATTNGHSOLFGHAKPGAPAIENETIPYTMTVPKDDGFLNGSC
SGLDBEASGSARPPPLLQEEWETVM"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755221.
                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-M942-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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                                                                                                           . Natl. Acad. Sci. ar{\mathbf{u}}.\mathbf{S.A.} 99 (26), 16899-16903 (2002)
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/clone_lib="NIH BMAP_FD0"
/lab_host="DH10B"
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/clone="MGC:62276 IMAGE:6402767"
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/db_xref="LocusID:19228"
/db_xref="MGI:97801"
/db_xref="MGI:97801"
/gene="Pthr1"
/codon_start=1
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/mol_type="mRNA"
/strain="C57BL/6"
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/gene="Pthr1"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (basea 1 to 2089)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Malek, J.A., Quarath, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wuzzy, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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ive 0; Mismatches 58;
                                         /clone="MGC:18447 IMAGE:4241234"
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/lab_host="DH10B"
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                     GGTGTCAGAGCAACCTTGGCCAACACTGGGTGCTGGGACCTGAGCTCTGGGCACAAGAAG 1136
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1 (bases 1 to 1380)

Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
PH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules
Patent: 19 2002533115-A 15 08-OCT-2002;
THE GENERAL HOSPITAL CORP
OS Artificial Sequence
N JP 2002533115-A/15
PD 08-OCT-2002
PP 30-DEC-1999 JP 2000591171
                                                                                ATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGCCAATGCGGGCCGGTGTGACACCAGG
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NRTWANY SECLKFMTNETREREVFDRLGMI YTVGYSMSLASLIVAVL I LAYFRRLHCT
RNY I HMHMFLSFMLRAASI FVKDAVLYSGFTLDEAERLTEEELHI I AQVPPPPAAAAV
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FVAVWGVRATLANTGCWDLSSGHKKWIJQVPILASVVLNFILFINIIRVLAFKLRET
NAGRCDTRQOYRKLLRSTLVLVPLFGVHYTVFWALPYTEVSGTLWQIQMHYEMLFNSF
OGFFVAIIXCFCNGEVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMGAHTSVTNV
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/db_xref="G1:474829"
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/product="parathyroid hormone/parathyroid hormone
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Pred. No. 1.8e-230;
0; Mismatches 59; Indels 0; C
                                                                                                                                                                                 /cell_type="embryonal carcinoma" <1. .1969
Direct Submission
Submitted (21-APR-1994) M. Karperien, T
Developmental, Biology, Uppsalalaan 8,
Location/Qualifiers
                                                                                            'organism="Mus musculus"
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/cell_line="P19 EC"
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/strain="C3H/HeHa"
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                                                                                                                                                             GCTCCCAAGGACGATGGGTTCCTCAACGGCTCCTGCTCAGGCCTGGACGAGGAGGAGGCCTCT
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                                               TITEGIGIGCACTACACCGICTICATGGCCTTGCCGTACACCGAGGTCTCAGGGACATTG
                                                                    TTTGGCGTCCACTACATTGTCTTCATGGCCACACATACACCGAGGTCTCAGGGACGCTC
                                                                                                                                        TGGCAGATCCAGATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTGTTGCC
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Description of Artificial Sequence: modified PTH receptor CC
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THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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86.8%;
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Best Local Similarity 86.8
Matches 1151; Conservative
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PTH functional domain conjugate peptides, derivatives thereof and
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BD266845.1 GI:33076613

JP 2002533115-A/14.

Synthetic construct

SWatchietic construct
other sequences, artificial sequences.

E 1 (bases 1 to 1380)

S gardellar.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.

PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules

L Patent: JP 2002533115-A 14 08-OCT-2002;

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OS Artificial Sequence

PN JP 2002533115-A/14
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PC C12N5/10, G01N33/15, G01N33/50, C12N15/00, C12N5/00, A61K37/02 CC
Description of Artificial Sequence: modified PTH receptor CC
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A61P19/10,
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                             CTCTTCAACTCCTTCCAGGGATTTTTTTTTGCCATCATATACTGTTTCTGCAATGGTGAG
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30-DEC-1999 JP 2000591171
31-DEC-1998 US 60/114577
THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Pred. No. 5.4e-195;
0; Mismatches 167;
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 84.8%;
Matches 1153; Conservative (
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RS Gardella, T.J., Kronenberg, H.M., Potts, J.T. and Jueppner, H. PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules

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OS ARTIficial Sequence
PN JP 2002533115-A 6 08-OCT-2002;

PR 31-DEC-1999 JP 2000591171

PR 31-DEC-1999 US 60/114577

PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI JUEPPNER
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                      1216 CITAACGGCTCCTGCTCAGGCCTGGATGAGGAGGCCTCCGGGTCTGCGCGGCCGCCTCCA 1275
                                                                                                                                                                                                                                                                                                                                                                         CTCAACGCTCCTGCTCAGGCCTGGACGAGGAGGCTCTGGGCCTGAGCGGCCACCTGCC 1320
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A61P19/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC
                                                                                                          AAGCGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGGTGTCTCACACG
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                                                                                                                                                                       CCTCCTGCCACTACCAATGGCCACTCCCAGCTGCCTGGCCATGCCAAGCCAGGGGCTCCA
                                                                                                                                                                                                                                                           GCCACTGAGAC -- - TGAAACCCTACCAGTCACTATGGCGGTTCCCAAGGACGATGGATTC
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                  Length 1380;
                    Score 977.8; DB 6; Length
Pred. No. 9.7e-194;
0; Mismatches 167; Indels
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                  Query Match
Best Local Similarity 84.5%;
Matches 1153; Conservative
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	OY 909 CTGTTTCTGCAATGGTGAGGCAGAGATTAGGAAGTCATGGAGCGGCTGGACACT 968	Qy 969 GGCGTTTGGACTTCAAGCCAAAGCACGAAGTGGGAGTAGCAGCTATGGCCCAAT 1028	OY 1029 GGTGTCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCTCCCCCTCAG 1088	OY 1089 CCCCGCACTGCCTCCTGCCACTACCAATGGCCACTCCCAGCTGCCTGGCCAA 1145	QY 1146 GCCAGGGGCTCCAGCCACTGAGACTGAAACCTACCGTCCCTATGGCGGCTTCCCAA 1202 Db 1645 GCCAGGGACCCCTGGAGACCCTGCAGACCCTGCCATGGCTGCTCCCAA 1704	QY 1203 GGACGATGCATAACGGCTCCTGCTCAGGCCTGGATGAGGAGCCTCCGGGTCTGC 1262 Db 1705 GGACGATGGGTTCCTCAACGGCTCCTGCTCAGGCCTGGAGCCTCTGGGCCTGA 1764	OY 1263 GCGGCCGCCTCCATTGTTGCAGGAAGGATGGGAAACAGTCATGTGACTGGGCACTAGG 1320	RESULT 14 AR270690 LOCUS LOCUS DEFINITION Sequence 1253 from patent US 6500938. ACCESSION AR270690 VERSION AR270690.	_	1 (bases Au-Young, Compositi Patent: U	BOUICE 1. 1948 /organism="unknown" /mol_type="genomic DNA"	Object Match 73.2%; Score 966.8; DB 6; Length 1948; Best Local Similarity 86.6%; Pred. No. 1.9e-191; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;	69 TGCGCTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCT 12	129 CGCTCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCGGCGGCTGCTTGCT	Qy 189 CAACTACATCCACATGTACTCCTGTCGTTATGCTGCGCGCGC	QY 249 GAAGGACGCTGTGCTCTGCGCTTCACGCTGGATGAGGCCGCGCCTCACAGAGGA 308

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                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                   Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors (GPCRS), antibodies thereto, and systems for identifying such antigenic peptides
Patent: WO 0206,1087-A 228 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
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    .1948
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

 GI:25813781
                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                       Best Local Similarity 86.6
Matches 1090; Conservative
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Search completed: July 4, 2005, 01:28:06 Job time : 5924 secs

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nucleic search, using sw model OM nucleic Run on:

July 3, 2005, 15:10:00; Search time 788 Seconds (without alignments) 9916.318 Million cell updates/sec

US-09-869-565-1

Title: Perfect score:

1 atgggggccgcccggatcgc.....tcatgtgactgggcactagg 1320 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

8780412 Fotal number of hits satisfying chosen parameters:

4390206 segs, 2959870667 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04: geneseqn1980s: Database :

genesegn2003cs:*genesegn2003ds:*genesegn2004as:* geneseqn2003as:* geneseqn2002bs: geneseqn2003bs: geneseqn2001as: geneseqn1990s:* geneseqn2000s:* geneseqn2001bs: geneseqn2002as:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:

Aaa51736 Human tet Aaa51737 Human tet Aaa51737 Human tet Aaa51734 Tethered Aba42719 Human par Aca56655 Human sig Adil3875 Osteoarth Adi56451 Human pol Adr47543 Human par Adq22747 Human sof Aav08391 Human Par Human pol Human par Human sof Abt42039 Toxicity Aaq29606 Rat bone Ado30323 Mouse GPC Aat15947 Rat bone Aav08390 Parathyro Adh61258 Rat bone Aaa58932 DNA encod Aaa51732 Tethered Description SUMMARIES ADH61258 ABT42039 AAQ29606 ADR47543 ADQ22747 AAV08391 ACA56655 ADL13887 ADL13875 ADI56451 AAA51735 AAA51737 AAA51732 AAT15947 AAV08390 AD030323 ABZ42719 AAA58932 AAA51734 Query Match Length DB 1948 2282 2010 2065 2051 1776 1380 1320 966.8 966.8 966.8 966.8 966.8 1241.6 1240 Score 1243.2 1243.2 966.8 1146.4 1006.4 Š. Result

Adh61259 Human PTH Ad71008 Human par Ad418188 Human sof Aa113876 Osteoarth Ad113876 Osteoarth Ad76824 Human wil Ab198021 Non-endog Ad30033 Human GPC Ad76391 Human PTH Aa35075 Human kid Aa425607 Human kid Aa425515 CDNA enco Abx15515 CDNA enco Adx15546 Opossum k Aav08389 Parathyro Ad161257 Opossum k	Aaq28605 Opossum k Aat15945 Opossum k Aav08388 Parathyro Adh61256 Opossum k Aaq28604 Opossum k Aaa30828 Zebrafish Aaa49625 Zebrafish Adc42304 CDNA enco Adh61058 Zebrafish
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ALIGNMENTS

DNA encoding a mutant parathyroid hormone (PTH) receptor. Mutant; parathyroid hormone; PTH; receptor; rdeltaNt; ligand binding domain; 88. Location/Qualifiers AAA58932 standard; DNA; 1320 BP. /*tag= b 67. .1305 /*tag= c (first entry) ಹ .1308 /*tag= 1. .66 /*tag= Homo sapiens 20-OCT-2000 sig_peptide mat_peptide AAA58932; čey RESULT 1 AAA58932

98WO-US027862. 98WO-US027862. WO200040698-A1 31-DEC-1998; 31-DEC-1998; 13-JUL-2000. #####X#X#X#X#X#X#X#X#X######

Potts JT; Gardella TJ, Kronenberg HM, (GEHO) GEN HOSPITAL CORP. WPI; 2000-465971/40. P-PSDB; AAB07529.

New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity.

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linked to a carboxy-terminal binding portion of parathyroid hormone for
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POTTS J T.
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P-PSDB; AAY96983.
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                                          The present sequence encodes a mutant parathyroid hormone (PTH) receptor, designated rdeltaNt. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists and
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tive 0; Mismatches
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                                           Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(-134) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inhalation unlike the large mative PTH or PTH-1 which avoids the need for regular injections to treat osteoporosis
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                       Claim 24; Fig 7; 119pp; English
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                                                CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCT
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                                                                                                                                                                                                                                                                 parathyroid hormone/parathyroid hormone-related professor (PTH/PTHFP) receptor (AAR92277). To obtain R15B, a rat osteosarcoma ROS 17/2.8 cDNA library in pcDNA1 was used to transfect COS cells, and transfectants were selected for ability to bind labelled PTH. Recombinant receptor is produced in vector/host cell systems. The host cells can be used for diagnostic measurement of PTH serum levels. Transgenic chickens that overaxpress the receptor in their oviduct lay eggs of higher calcium content. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTGGGGCTTCACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTGTGGGTC 1092
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                                                                                                                                                            parathyroid hormone receptor - useful for of e.g. hypercalcaemia, hypo-calcaemia, cancer
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                                                                                                                                                                                                                                                       (AAT15947), designated R15B ATCC 68571, codes for a rat
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2051;
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                                                                  Kronenberg HM;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;
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                                                                 Schipani E,
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                        Claim 1; Fig 3A-3E; 64pp; English.
                                                                 Segre GV,
    91US-00681702
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.8%;
Matches 1245; Conservative
                                                                                                                                                            DNA encoding vertebrate diagnosis and treatment
                                                                 Potts JT, Juppner H,
Abou-Samra A;
                                  (GEHO ) GEN HOSPITAL
                                                                                                              WPI; 1996-139028/14
                                                                                                                             P-PSDB; AAR92277
                                                                                                                                                                                                                                                       A cDNA clone
    05-APR-1991;
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                ATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTTGTTGCCATCATATACTGT
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73. 1848
/*tag= a
/product= "Rat bone PTH/PTHrP receptor protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat bone PTH/PTHrP receptor cDNA clone, R15B.
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92US-00864475.
95US-00471494.
98US-00199874.
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06-APR-1992;
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                                                                                                                                                                                      This sequence encodes the rat parathyroid hormone (PTH) receptor RiSB, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia
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                                                                                            New isolated DNA encoding parathyroid hormone receptor polypeptides, useful for diagnosing and treating disorders associated with parathy
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0; Mismatches
                                                                                                                                                                     Claim 3; SEQ ID NO 3; 71pp; English
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99.8%;
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Matches 1245; Conservative
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94.1%; Score 1241.6; DB 10; Length 2065;
Best Local Similarity 99.7%; Pred. No. 2.8e-314;
Matches 1244; Conservative 0; Mismatches 4; Indels 0; 0
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2001US-0330867P.
2001US-0331805P.
2001US-0336144P.
2001US-0340873P.
2002US-0357842P.
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2002US-0357844P.
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01-NOV-2001; 2
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21-FEB-2002; 2
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                                   TGCCGCGTGGCGGTGACCTTCCTTCCTTCTTCCTGGCTACCAACTACTACTGGATCCTG
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93.9%; Score 1240; DB 2;
Best Local Similarity 99.6%; Pred. No. 5.7e-314;
Matches 1243; Conservative 0; Mismatches 5;
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                                                                                          Location/Qualifiers
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P-PSDB; AAR27706.
                        hypercalcaemia; ss.
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Schipani E;
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29-JUL-2004 (first entry)

Mouse GPCR PTHR1 polynucleotide, SEQ ID NO:1426.

Transgenic mouse; neurological disorder; adrenal gland disorder;

transgenic mouse; neurological disorder; adrenal gland disorder;

colon disorder; neurological disorder; adrenal gland disorder;

where the disorder; blood disorder; immune disorder; bone disorder;

y joint disorder; liver disorder; nutritive disorder; cancer;

whinty disorder; liver disorder; nutritive disorder; cancer;

whint disorder; uterus disorder; prostate disorder; spleen disorder;

skin disorder; stomach disorder; pancreas disorder; spleen disorder;

thymus disorder; thyroid disorder; antiparkinsonian; antimanic;

cytostatic; antimilammatory; vasotropic; antianginal; antiarrhythmic;

cytostatic; antimilammatory; vasotropic; antianginal; antiarrhythmic;

whint disorder; antibacterial; antianaemic; antiseborrhoeic;

dermatological; antiulcer; antithyroid; antiallergic; anorectic;

wimmunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;

wmutine; gene; se.

Mus musculus.

WO20040400000-A2

13-MAY-2004.

13-FM1-2004.

09-SEP-2003; 2003WO-US028226

09-SEP-2002; 2002US-0409303P-09-APR-2003; 2003US-0461329P-

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F; Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;

WPI; 2004-390329/36: P-PSDB; ADO29629.

Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 151; SEQ ID NO 1426; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR.related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising of GPCR gene of the invention; a mouse comprising of mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived to probes which hybridise to GPCR polymucleotides of the invention. The comprising a mutation in a different GPCR polymucleotides of the invention. The comprising a mutation further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid The GPCR polypeptides and vectors comprising a GPCR nucleic acid The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, disease, disorders of the colon or intestine of disorders of the adrenal gland; disorders of the colon or intestine of sorders of the adrenal gland; disorders of the colon or intestine of syndrome); cardiovascular disorders (e.g., autoimmune disorders or mycardial infarction); immune disorders (e.g., autoimmune disorders or AlDS); bone and joint disorders (e.g., autoimmune disorders (e.g., autoimmune disorders (e.g., autoimmune disorders (e.g., cancais and disorders of the kidney, liver, lung, breast, ovary, chencing diseases); and disorders of the kidney, liver, lung, breast, covary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-related

1140 ö 1380 GGTGTCAGAGCAACCTTGGCCAACACTGGGTGCTGGGACCTGAGCTCTGGGCACAAGAAG 1080 1200 TTCTGCAATGGTGAGGTGCAGGCAGAGATTAGGAAGTCTTGGAGCCGCTGGACACTGGCA 1440 132 9 192 9 840 432 960 552 612 1261 TACACCGTCTTCATGGCCTTGCCGTACACCGAGGTCTCAGGGACACTGTGGCAGATCCAG 1320 TTGGACTTCAAGCGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1032 252 720 312 780 372 900 GTGGAGGGCTGTACTTGCACAGCCTCATCTTCATGGCCTTTTTCTCAGAGAAGAAGTAC 492 672 732 792 852 912 972 nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at TCCCTCACCGTGGCTGTGCTCATCCTAGCCTATTTTAGGCGGCTGCACTGCACGCGCAAC GTGGAGGGACTGTACTTACACAGCCTCATCTTCATGGCCTTTTTTCTCAGAGAAGAAGTAT CTGTGGGGCTTCACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTGGGGTC 541 CGGGAGGTATTTGACCGCCTGGGCATGATCTACACCGTGGGATATTCCATGTCTTGCC GACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCCGAGCGCCTCACAGAGGAGGAGAG GACGCTGTGCTCTTGGCTTCACGCTGGATGAGGCCCGAGCGCCTCACGGAGGAGAG TTGCACATCATCGCGCAGGTGCCACCTCCGCCGGCCGCTGCCGCCGTAGGCTACGCTGGC Triccaratricarcicided de descripte de la contraction de la contract TCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCGCAAC TGCCGCGTGGCGGTGACCTTCTTCCTTCTTCCTGGCTACCAACTACTACTGGATCCTG GGTGTCAGAGCAACCTTGGCCAACACTGGGTGCTGGGATCTGAGCTCCGGGCACAAGAAG 1081 regarcarccaegreccearccrescarcrestrerereactrearcrererranceac 1141 ATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGCAATGCGGGCCGGTGTGACACCAGG CTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCC TGGATCATCCAGGTGCCCATCCTGGCATCTGTTGTGCTCCAACTTCATCCTTTTATCAAC ATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATGCGGGCCGGTGTGACACCAGG CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTTGGTGTGCAC ATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTGTTGCCATCATATACTGT Arecacrareagarecrericaacrecrrecaecearrirricireccareararacrer TTCTGCAATGGTGAGGTGCAGGCAGAGATTAGGAAGTCATGGAGCCGCTGGACACTGGCG Gaps Length 1776; ; 0 Sequence 1776 BP; 364 A; 519 C; 500 G; 393 T; 0 U; 0 Other; 56; Indels Score 1146.4; DB 12; Pred. No. 1.6e-289; 0; Mismatches 56; II ftp.wipo.int/pub/published_pct_sequences. 86.8%; 95.5%; Conservative Best Local Similarity Matches 1180; Conserv 73 133 601 193 661 253 721 313 781 373 841 433 901 961 553 1021 613 673 853 1321 1381 493 733 793 913 973 Query Match 8888888 셤 ઠે 용 셤 셤 g g a ઠ à ઠે ð ò 원 ò ઠે 셤 ò ઠે 용 ઠે 용 à 셤 ò a ò 엄 δ 셤 ò ä

Gaps

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420 441 480 501 540 561 600 621 99 681 720 741

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portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, tracting diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH PW which avoids the need for regular injections to treat osteoporosis
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Pred. No. 6.3e-253;
0; Mismatches 166; Indels 12;
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Matches 1148; Conservative
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                                                     GCACACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCCTTCCCCTTAGCCCC
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JUEPPNER H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
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                                                                                                          New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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                                                                                                                                                                                                                                                          Example 4; Fig 17; 119pp; English
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Matches 1152; Conservative
WPI; 2000-452384/39.
P-PSDB; AAY96986.
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Potts JT,
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WO200039278-A2
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                                         CCCATCCTGGCCTCCATTGTGCTCAACTTCATCCTCTTCATCAATATCGTCCGGGTGCTC 720
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CTGGCCAACACCGGGTGCTGGGACTTGAGCTCCGGGAACAAAAAGTGGATCATCCAGGTG 660
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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or inchalation unlike the large native PTH or PTH-1 which avoids the need for regular injections to treat osteoporosis
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compound comprising an amino terminal signaling functional domain ted to a carboxy-terminal binding portion of parathyroid hormone for thing mammalian conditions characterized by decreases in bone mass.
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PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
PTH-1 receptor; resorption; remodeling; r-delta-NT/Ct; tethered receptor;
osteoporosis; ss.
 Tethered PTH-1 receptor, r-del-Nt/Ct coding sequence.
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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R or S-(L
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psoriasis, anxiety, depression, schizophrenia, dementia, memory loss, mental retardation; epilepsy; asthma, tuberculosis, obesity, nausea; hypertension, hypotension, renal disorder, rheumatoid arthritis, trauma,

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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, immunological-related cell proliferative GPCRs and antibodies immune diseases, eg. ALDS, Alzheimer's disease, atherosclerosis, bacterial, fungal protozoan or viral infections, atherosclerosis, bacterial, fungal protozoan or viral infections, correctivities, osteoprososis, cancer, cardiomyopathy, chonic and acute inflammation, allergies, Crohn's disease, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, concertivities, trauma, ulcers, or hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or sepilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or sepilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or sepilepsy, and multiple sclerosis, pain, bypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or used in immunoassays and immunodiagnosis. ABS42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the prese New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AlDS, Alzheimer's disease, cancer or 128 248 624 129 CGCCTCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCG 188 684 744 CAACTACATCCACATGCACCTGTTCCTGTCCTTCATGCTGCGCGCGGTGAGCATCTTCGT TGCGCTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCT reaaceesasererricacceceresecarearriaracacceresecracicererrerr gecerceceraecrerecrearceresecraerrinasecsecreeaedes . 9 Length 1948; Sequence 1948 BP; 405 A; 600 C; 570 G; 373 T; 0 U; 0 Other; Indels DB 8; 0; Mismatches 162; Score 966.8; DB 8, Pred. No. 1.7e-242 Disclosure, Fig 1; 523pp; English. (LIFE-) LIFESPAN BIOSCIENCES INC. 19-DEC-2000; 2000US-0257144P. 19-DEC-2001; 2001WO-US050107 73.2%; 86.6%; Conservative Roush CL, WPI; 2003-046718/04. autoimmune diseases. Query Match Best Local Similarity Matches 1090; Conserv P-PSDB; ABP81872. WO200261087-A2 08-AUG-2002 Burmer GC, 69 565 625 189 셤 용 ò ₽ g

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G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

Human parathyroid hormone receptor 1 nucleotide SEQ ID NO:228

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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnostics and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, corensists and paramacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a suppopulation of mansa. The array can detect changes in expression in a large number of genes coding carray can detect changes in expression in a large number of genes coding various diseases including cancer e.g. adenocarcinoma and leukaemia, cumunopathise e.g. AlDS and asthma, neuropathise e.g. AlDS and asthma, neuropathise e.g. Alzheimer's disease and parkinson's disease. The present sequence represents a polynucleotide format directly from USPTO at the printed sepecification but was obtained in electronic condess when the directly from USPTO at the procession of the printed specification but was obtained in electronic procession and lacetly and new condession and lacetly and new condession and lacetly and new condession and detect condession and asthma.
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signalling pathway population; cancer; adenocarcinoma; leukaemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
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86.6%; Pred. No. 1.7e-242;
cive 0; Mismatches 162;
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The invention relates to a method of determining susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain comprising identifying whether the individual has at least one polymorphism in a polymotheride encoding at least one of the protein listed in the specification. The methods, composition and agent are useful for modulating the susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain that is associated with a disease, preferably osteoarthritis. The cell line and the non-human animal are useful for screening for an agent for diagnosing an individual having susceptibility to joint space narrowing and/or osteophyte development and/or joint pain. This sequence corresponds to the polymodeotide encoding a protein listed in the specification. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polymucleotide encoding
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0; Mismatches 162;
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                                                                                                                                                                                           polymorphic
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Matches 1090; Conservative
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Search completed: July 3, 2005, 23:49:25 Job time : 798 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Minimum DB Maximum DB

Database :

Result

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94.2%; Score 1243.2; DB 1; Length 2051;
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APPLICANT: Segre, Gino V.
APPLICANT: Shou-Samar, Abdul-Badi
APPLICANT: Abou-Samar, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF INVENTION: AND DNA ENCODING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                              US-08-811-897A-31

US-08-852-213-31

US-09-201-474-31

US-08-811-897A-39

US-08-85-213-39

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US-08-453-956-14
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US-08-811-897A-40
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US-08-855-213-32
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STATE: Massachusetts
COUNTRY: 10.5.A.
ZIP: 0.2110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/07/664,475A
FILING DATE: 04-06-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/681,702
FILING DATE: 05-04-1991
ATTORNEY/AGNIT INFORMATION:
NAME: PAUL T. CLARK
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REERERONG/COCKET NUMBER: 07/681,702
TELEPRAN: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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TOPOLOGY:
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-016-434-1253
US-08-468-249A-4
US-09-826-509-562
US-07-864-475A-2
US-08-468-249A-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length
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                                                                                                          GCTCCAGCCACTGAGACTGAAACCCTACCAGTCACTATGGCGGTTCCCAAGGACGATGGA
                                              CTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCC
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                                                                                                                                                 Sequence 3, Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-AAY-1991
ATTORNEY/AGENT INPORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617/542-5070
TELEPAX: 617/542-8006
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 1245; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: MA
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; LOCATION:
US-08-468-249A-3
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                                                                                                        TCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCGCAAC 192
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                  3; Indels
   Pred. No. 0;
0; Mismatches
   99.88;
                  Matches 1245; Conservative
    Similarity
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Db 1753 TTCCTTAACGGCTCCTGGCTGGATGAGGAGGCCTCCGGGTCTGCGCGCCGCT 1812 Oy 1273 CCATTGTTGCAGGAAGGATGGGAAACAGTCATGACTGAGCACTAGG 1320	RESULT 3 US-09-016-434-1253 Sequence 1253, Application US/09016434 ; Batent No. 6500938 ; GENERAL INFORMATION: APPLICAMT: Jaffron, 1 Soilbang	NVENTION: COMPOSITION FOR NVENTION: PATHWAY GENE EXPISEQUENCES: 1490	ä"ab	; CONTRY: USA; ZIP: 943.04; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk.	P # P 0	FEFICATION NUMBER: US/US/US/US/US/US/US/US/US/US/US/US/US/U	รีย์สือ	REGISTRATION NUMBER: 37,071 REFERENCE/DOCKET NUMBER: PA-0002 US TELECOMMUNICATION INFORMATION:	ž " 5		; INTELLATE CENTRAIN ; LIBRARY: GENBANK ; CLONE: 9190721 US-09-016-434-1253	Query Match 73.2%; Score 966.8; DB 4; Length 1948; Best Local Similarity 86.6%; Pred. No. 2.1e-256; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;	Qy 69 TGCGGTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCT 1.28	Qy 129 CGCCTCCCTCACGGTGGCTGTGCTCATCGTGGCCGTATTTTAGGCGGCTGCACTGCACTGCACGGGGGTBB	Oy 189 CAACTACATCATGACATGTTCCTGTCGTTTATGCTGCGGCGGGGGCATCTTCGT 248	Qy 249 GAAGGACGCTGTGCTCTACTCTGGCTTCACGGTGGGATGAGGCCGGCC
673 TCCTCACGGTGGCTGTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCGAAC 732 193 TACATCACATGCACATGTTCTGTCGTTTATGCTGCGCGGAGCATTTTGTGAAGAACATTGTTAGAAAAAAAA	253 GACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGAGCGCCTCACAGAGGAGGAGGGGGCTCACAGAGGAAGAG 312 193 GACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGAGCGCCTCACAGAGGAAGAG 852 313 TTGCACATCATCGCGAGGGCACCTCCGCCGGCGCCGTGCCGTAGCTACGCTGGC 372 11	TGCCGCGTGGCGGTGCCTTCTTCCTCTCTGCCTGCCGCTGCCGCTACTACTACTGGTGCCTG	433 GTGGAGGGCTGTACTTGCACAGCCTCATCTTCATGGCCTTTTTCTCAGAGAAGAAGTAC 492 	493 CTGTGGGGCTTCACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTGTGGGTC 552 	553 GGTGTCAGAGCAACCTTGGCCAACACTGGGTGTTCTGAGCTCCGGGCACAAGAAG 612 	613 TGGATCATCCAGGTGCCCATCCTGGCATCTGTTGTGCTCAACTTCATCCTTTTTATCAAC 672 	673 ATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATGCGGGCCGGTGTGACACCAGG 732 	733 CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTCGCCGCTCTTTGGTGTGC 792 	793 TACACCGTCTTCATGGCCTTGCCGTACACCGAGGTCTCAGGGACATTGTGGGCAGATCCAG 852 	853 AIGCATTAIGAGAIGCTCTTCAACTCCTTCCAGGGAITTTTTGTTGCCATCATATACTGF 912 	913 TTCTGCAATGGTGGAGGCAGGCAGAGATTAGGAAGTCATGGAGCCGCTGGACACTGGCG 972 	973 TTGGACTTCAAGCGCAAAGCACGAAGTGGAAGTAGCAGCTACAGCTATGGCCCAATGGTG 1032 	1033 TCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCCTCCCCCTCAGCCCC 1092	1093 GGCTGCCTCCTGCCACTACCAATGGCCACCTGCCTGGCCATGCCAAGCCAGG 1152 	1153 GCTCCAGCCACTGAGACTGAAACCCTACCGGTCACTGGCGGTTCCCAAGGACGATGGA 1212 	1213 TTCCTTAACGGCTCCTGCTCAGGCCTGGATGAGGAGGCCTCCGGGTCTGCGCGGCCGCCT 1272

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Sequence 4, Application US/07864475A Patent No. 5494806 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   3: Fish & Richardson
225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 86.6
Matches 1089; Conservative
                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-07-864-475A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2010
                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 22
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       745 CAAGGACGCTGTGCTCTACTCTGGCGCCACGCTTGATGAGGCTGAGCGCCTCACCGAGGA 804
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                                                                                 805 GGAGCTGCGCGCATCGCCCAGGCGCCCCGCCGCCGCCACCGCCGCTGCCGCTACGC
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                                                    369 TGGCTGCCGCTGGCGGTGACCTTCTTCCTTCCTGGCTACCAACTACTACTGGAT
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128 623 188 683 248 743 308 803 368 428 804 edadoridos de controdos de contratos de 684 CAACTACATCCACATGCACCTGTTCCTGTCCTTCATGCTGCGCGCGTGAGCATCTTCGT 369 TGGCTGCCGCGTGGCGTGACCTTCTTCCTCTACTTCCTGGCTACCAACTACTGGAT TGCGCTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCT 129 GCCTCCCTCACGGTGGCTGTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCG CAACTACATCCACATGCACATGTTCCTGTCGTTTATGCTGCGCGCCGCGAGCATCTTCGT GAAGGACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCCGAGCGCCTCACAGAGGA 744 CAAGGACGCTGTGCTCTACTCTGGCGCCACGCTTGATGAGGCTGAGCGCCTCACCGAGGA Gaps . 9 Length 2010; Indels APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Juppner, Harald
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 73.1%; Score 965.2; DB 1; 86.6%; Pred. No. 5.9e-256; iive 0; Mismatches 163; COUNTRY: U.S.A.

ZITP: 0.110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A

FILING DATE: 04-06-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/681,702

FILING DATE: 05-04-1991
ATTORNEY/AGENT INFORMATION:
NAME: PAUL CLARK
REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/071002

TELEPHONE: (617) 542-5070

'n

RESULT 4 US-07-864-475A-4

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Pish & Richardson P.C. 225 Franklin Street

RY: USA 02110-2804

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/864,475
PRIOR APPLICATION NUMBER: US 07/864,475
PRIOR APPLICATION NUMBER: US 07/861,702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/22.
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
TRNGTH: 2010 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2010 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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                   STREET: 225 | CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-468-249A-4
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                                                            924 TCTGGTGGAGGGCTGTACCTGCACGCCTCATTTTATGCCTTCTTCTCAGAGAAA 983
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                                   Gaps
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   Length 2010;
                                 Indels
 Score 965.2; DB 2;
Pred. No. 5.9e-256;
0; Mismatches 163;
Query Match 73.1%;
Best Local Similarity 86.6%;
Matches 1089; Conservative (
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Sequence 4, Application US/08468249A

Patent No. 5886148

GENERAL INFORMATION:

APPLICANT: Segre et al., Gino V.

TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLES OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

US-08-468-249A-4

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596 188 929 248

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                                                                                 Query Match 72.7%;
Best Local Similarity 86.8%;
Matches 1081; Conservative
  PatentIn Version
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                                 TYPE: DNA
CRGANISM: Homo
US-09-826-509-562
SOFTWARE: Pater
SEQ ID NO 562
LENGTH: 1782
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; Sequence 562, Application US/09826509
; Sequence 562, Application US/09826509
; Patent No. 6806054
; Patent No. 6806054
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Protein-Coupled Receptors
; TITLE OF INVENTION: Protein-Coupled Receptors
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: ARRN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
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  GTACCTGTGGGGCTTCACAGTCTTCGGCTGGGGTCTGCCCGCTGTCTTCGTGGCTGTGTG 1043
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GGCGTTGGACTTCAAGGGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAAT 1028 CCAGATGCACTATGAGATGCTCTTCAACTCCCTTCCAGGATTTTTTGTCGCAATCATATA 1376 1257 ccacracarrercrrcaregecacacacaracaceaagarercagagagecreregeaagr 1316 597 GGCGTCCCTCACCGTAGCTGTGCTCTTGGCCTACTTTAGGCGGCTGCACTGCACGCG CGCCTCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCG CAACTACATCCACATGCACATGTTCCTGTCGTTTATGCTGCGCCCCGCGAGCATCTTCGT GNAGGACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCCGGAGCCCTCACAGAGGA 717 CAAGGACGCTCTGCTCTCTCGCCCCACGCTTGATGAGGCTGAGCGCCTCACCGAGGA 777 GGAGCTGCGCCCATCGCCCCAGGCGCCCCCCCCCCCCTGCCACCGCCGCTGCCGGCTACCG 19GCTGCCGCGTGGCGGTGACCTTCTTCTTACTTCCTGGCTACCAACTACTACTGGAT 837 gescriccaecererereaccrirerrecriracrirecresecaecaecraeracresear GTACCTGTGGGGCTTCACCATCTTTGGCTGGGGTCTACCGGGCTGTCTTCGTGGCTGTGTG GGTCGGTGTCAGAGCAACCTTGGCCAACACTGGGTGCTGGGATCTGAGCTCCGGGCACAA 609 GAAGTGGATCATCCAGGTGCCCATCCTGGCATCTGTTGTGCTCAACTTCATCCTTTTTAT CAACATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGCCAATGCGGGCCGGTGTGACAC CAGGCAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTGGTGT CCAGATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTGTTGCCATCATATA CTGTTTCTGCAATGGTGAGGTGCAGGCAGAGTTTAGGAAGTCATGGAGCCGCTGGACACT TGCGCTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCT CAACTACCATCCACATGCACCTGTTCCTGTTCCTTCATGCTGCGGCGGCGTGAGCATCTTCGT CCTGGTGGAGGGGCTGTACTTGCACAGCCTCATCTTCATGGCCTTTTTCTCAGAGAAA 9 Length 1782; Indels Score 959.6; DB 4; Pred. No. 1.9e-254; 0; Mismatches 159;

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GTGGAAGGCCTCTACCTTCACAGCCTCATCTTCATGGCTTTTTTTCTCTGAGAAAAAGTAT 1039
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                                                                                                                                     133 TCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACGCGCCAAC
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                                                            CTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCC
                                                                                      CGGGAAGTCTTTGATCGCCCTCGGAATGATCTACACTGTGGGCTACTCCATCTCTCTGGGC
                                                                                                                                                                                                                 TACATCCACATGCACATGTTCCTGTCGTTTATGCTGCGCGCCGCGCGCATCTTCGTGAAG
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                      Indels
    Pred. No. 1.7e-180;
0; Mismatches 294;
  74.2%;
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                                                                                                                 GGTGTCCCACACACAGGTGTGACCAATGTCGCCCCCGTGTGGGGACTCGGCCTCGCCCCTCAG
                                      GGTGTCTCACACGAGTGTGACCAATGTGGGCCCCCCGTGCAGGACTCAGCCTCCCCCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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ZIP: 0110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,475A
FILING DATE: 04-06-1992
CLASSIFTCATION DATA:
APPLICATION NUMBER: 07/681,702
FILING DATE: 05-04-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.4%; Score 691.6;
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ER: 00786/071002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07864475A Patent No. 5494806 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEI/AUGUT CLEIK
NAME: PRULT CLEIK
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAK: (617) 542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COUNTRY: U.S.A.
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STRANDEDNESS: double
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TCCCTCACTGTGGCTGTGTGTGTTTTGGGTTTAGGAGGTTACATTGCACCCGAAAC
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                                                                                                                                                                                                                            CGACTAGCTCCTGGGGCTGGAGCCAGTGCCAATGGCCATCACCAGTTGCCTGGCTATGTG 1699
                                                                AAGCCAGGGGTTCCAGCCACTGAGACTGAAACCCTACCAGTCACTATGGCGGTTCCCAAG 1203
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                                                                                                                                                                                                                                                                                                                    CAGCCCCTCCACTCCTGGAGGAGGAGAGAGAGACAGTCATGTGAC 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
COMMESSPONDENCE ADDRESS:
ADDRESSPONENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-APR 1991
ATTORNEY/AGENT INFORMATION:
NAME: Frager, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 691.6; DB 2;
Pred. No. 1.7e-180;
0; Mismatches 294;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
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Best Local Similarity 74.2%;
Matches 925; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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98..1853
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ZIP: 02110-2804
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US-08-468-249A-2
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LOCATION:
US-08-468-249A-2
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STATE:
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; Sequence 1, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION:
; FILE REFERENCE: 0609.4740001/SRL/M-G
                                                                                                                                                                                                                    553 GGTGTCAGAGCAACCTTGGCCAACACTGGGTGCTGGGATCTGAGCTCCGGGCACAAGAAG
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                                                                                                   HORMONE RECEPTOR AND
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Fatentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 05/08/468,249A FILING DATE: 06-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 51.6%; Score 681.2; DB 2; Best Local Similarity 74.2%; Pred. No. 1.3e-177; Matches 925; Conservative 0; Mismatches 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00786/071003
          Sequence 1, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
    APPLICANT: Segre et al., Gino V.
    TITLE OF INVENTION: PARATHYROID HORMO;
    TITLE OF INVENTION: ENCODING SAME
    NUMBER OF SEQUENCES: 21
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION UNBER: US 07/681,702
APPLICATION UNBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00'
TELECOMMUNICATION: INFORMATION:
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TELEPHONE: 617/542-5070
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TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
TELEPHONE: 1862 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION:
US-08-468-249A-1
        US-08-468-249A-1
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TGGTGTCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCCTCCCCCTCA 1087
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                                                                                                                                  TGGCGTTGGACTTCAAGCGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Soppet, Daniel R
APPLICANT: Y1, Li
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor TITLE OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 387.4; DB 3;
Pred. No. 1.5e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/468,011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08468011A; Patent No. 6030804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEFHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2003 base pairs
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ilarity 64.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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nes 612; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                         Score 554.6; DB 4;
Pred. No. 9.9e-143;
); Mismatches 304;
CURRENT APPLICATION NUMBER: US/09/449,632
CURRENT FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: US 60/110,467
PRIOR FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 1
LENGTH: 1609
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Best Local Similarity 70.7%;
Matches 756; Conservative
                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)..(1608)
US-09-449-632-1
                                                                                                                                                                       TYPE: DNA
ORGANISM: zebrafish
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Score 387.4; DB 3; Pred. No. 1.5e-96; 0; Mismatches 326;

Length 2003;

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                                                                                                                                               Match 29.3%;
Local Similarity 64.6%;
les 612; Conservative
                                        TYPE: DNA
CRGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (90)..(1715)
US-09-236-468A-1
    PatentIn Ver.
   SOFTWARE: Pate
SEQ ID NO 1
LENGTH: 2003
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                                                                                                                                                                                           TGACCCACAAAATTCCATTGAGGCAACTTCTGTGGACAAATC-----ACAATATATCGG 793
TICCTTGGCTGTGGCTATTCTCATCATTGGTTACATTGCATTGCATTGCACTAGGAA
                                                               CTATATICCACATGCACTTATITGTGTCTTTCATGCTGAGAGCTACAAGCATCTTTGTCAAA
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                                              CTACATCCACATGCTCCTGTCGTTTATGCTGCGCGCCGCGAGCATCTTCGTGAA
                                                                                                        GGACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGAGCGCCTCACAGAGGAAGA
                                                                                                                                                                GTTGCACATCATCGCGCAGGTGCCACCTCCGCCGGCCGCTGCCGCCGTAGGCTACGCTGG
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US-09-236-468A-1
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Sequence 1, Application US/09236468A
Batent No. 6338951
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
FILE REPERENCE: PP201D1
CURRENT APPLICATION NUMBER: US/09/236,468A
CURRENT FILING DATE: 1999-01-25
FRIOR FILING DATE: 1999-01-25
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
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974 TGTGGCACGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACTTAGTGCTGGAGACATCAA 1033
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                                              740 TGACCCACAAAATTCCATTGAGGCAACTTCTGTGGACAAATC----ACAATATATGGG 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 GTTGCACATCATCGCGCAGGTGCCACCTCCGCCGGCCGCTGCCGCCGTAGGCTACGCTGG
                                                                                              CTGCCGCGTGGCGGTGACCTTCTTCCTCTACTTCCTGGCTACCAACTACTACTGGATCCT
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Patent No. 6541220
GENERAL INFORMATION:
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ORGANISM: zebrafish
FEATURE:
NAME/KEY: CDS
LOCATION: (394)...(2019)
NAME/KEY: misc. feature
LOCATION: (2125)...(2125)
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LENGTH: 2152
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                        972 GTTGGACTTCAAGCGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCT 1018
                                                   1391 CGTGGAAAAAGGACACCGCCATGTGGCAGCCGCAGATGCGGCT 1437
                                                                                                                                                                                                                             APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
TITLE OF INVENTION: HLTDG74
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ZIP: 07068-1739

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07085
FILING DATE: 05-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-393
TELECOMMUNICATION NIFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1705
TELEPAX: 201-994-1705
TELEPAX: 201-994-1705
TELEPAX: 201-994-1705
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Oletein
STREET: 6 Becker Farm Road
CITY: Roseland
                                                                                                                                                                               Sequence 1, Application PC/TUS9507085
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, E
ADDRESSEE: Stewart &
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MOLECULE TYPE: cDNA
FEATURE:
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COUNTRY: U
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; LOCATION:
PCT-US95-07085-1
                                                                                                                                          RESULT 14
PCT-US95-07085-1
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                                                                                 Gaps
                                                                                 45;
                                                 Length 2152;
                                                                               0; Mismatches 276; Indels
; OTHER INFORMATION: n is any nucleotide of a,t,g or US-09-449-632-3
                                               Score 387.4; DB 4;
Pred. No. 1.5e-96;
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                                               29.3%;
                                                              Best Local Similarity 65.4 Matches 608; Conservative
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Sequence 1, Appli Sequence 2, Appli Sequence 1564, A

Sequence 2, Appli Sequence 1, Appli Sequence 22, Appli Sequence 1, Appli Sequence 52, Appli Sequence 52, Appli Sequence 1, Appli

Sequence 1, Appli Sequence 3, Appli Sequence 226, App Sequence 525, App Sequence 1463, Ap Sequence 70, Appl Sequence 2138, Ap Sequence 6394, Ap Sequence 564, App Sequence 564, App Sequence 564, App

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Database

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Sequence 3, Application US/10267730;
Sequence 3, Application US/10267730;
Publication No. US20030153041A1;
GENERAL INFORMATION:
APPLICANT: Segre, Gino V.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Orlus, Harry M.
APPLICANT: Orlus, Harry M.
APPLICANT: Orlus, DANATHROID HORMONE RECEPTOR AND DNA ENCODING SAME
TITLE OF INVENTION PRAINTROID HORMONE RECEPTOR AND DNA ENCODING SAME
FILE REFERENCE: 00786/071005;
CURRENT FILING DATE: 1995-06-06
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 3
LENGTH: 2051
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10 US-10-955-095-62

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1 US-10-943-446-1

US-09-943-446-1

US-09-944-446-1

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Pred. No. 0;
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LOCATION: (73)...(1845)
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Sequence 5, Appli
Sequence 228, Appl
Sequence 1253, Appl
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MBW_PUB.seq:*
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US-10-305-720-1253
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                        GenCore version
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Maximum Match 100%
Listing first 45 summaries
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Score

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                                      CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTGGTGTCCAC
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                                                                                                                      ATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTTGTTGCCATCATATACTGT
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Patent No. US20020146777A1

GENERAL INFORMATION:
APPLICANT: Peizer Inc.
APPLICANT: Lu, Bihong
APPLICANT: Lu, Bihong
APPLICANT: Lu, Bihong
APPLICANT: Smock, Steven L.
ITILB OF INVENTION: Canine Parathyroid Hormone 1 Receptor
FILE REFERENCE: PC10891AGPR
CURRENT APPLICATION NUMBER: US/09/943,446
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/229,170
PRIOR APPLICATION NUMBER: US 60/229,170

PRIOR APPLICATION NUMBER: US 60/229,170

PRIOR APPLICATION NUMBER: S001-08-30

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 4
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86.8%; Score 1146.4;

Best Local Similarity 95.5%; Pred. No. 0;

Matches 1180; Conservative 0; Mismatches
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Sequence 228, Application US/10225567A

Sequence 228, Application US/10225567A

Sequence 228, Application No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
FRIOR PILING DATE: 2000-12-19
FRIOR PILING DATE: 2000-12-19
SOFTWARE: PETCALION NUMBER: 60/257,144
FRIOR PILING DATE: 2000-12-19
SOFTWARE: PETCALION VERSION 3.1
SEQ ID NO 228
LENGTH: 1948
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US-09-943-446-5

Sequence 5, Application US/09943446

Patent No. US20020146777A1

GENERAL INFORMATION:

APPLICANT: Castleberry, Tessa A.

APPLICANT: Lu, Bihong

APPLICANT: Smock, Steven L.

TITLE OF INVERTION: Canine Parathyroid Hormone 1 Receptor FILE REFERENCE: PC10891AGPR

CURRENT APPLICATION NUMBER: US/09/943,446

CURRENT PILING DATE: 2000-08-30

PRIOR APPLICATION NUMBER: US 60/229,170

PRIOR PILING DATE: 2000-08-30

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1

SEQ ID NO 5.
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                                                                    CCATTGTTGCAGGAAGGATGGGAAACAGTCATGTGA 1308
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95.5%; Pred. No. 0;
ive 0; Mismatches
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Matches 1180; Conservative
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ORGANISM: Homo Sapiens
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Query Match 73.2%; Score 966.8; DB 15; Length 1948; Best Local Similarity 86.6%; Pred. No. 3.4e-285; Indels 6; Gaps 2; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Conservation 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Conservation 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Conservation 0; Mismatches 162; Indels 6; Gaps 2; Matches 1090; Mismatches 1090; Mismatches 1090; Mismatches 1090; Mismatches 1090; Matches 1090; </td <td>GARGENGECTSTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGAGGGCCTCACAGAGGA A AAAGTTGCACATTGCTCACTCTGCCTCCACGCTGGATGAGGCCTGCCGAGGAGGAGGAGGAGGAGGAGGCCTGCCGAGGAGGAGGCCTGCCGAGGAGGAGGCCTGCCGGCTACCGCTACCAGGAGGAGGCCCCCCCC</td>	GARGENGECTSTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGAGGGCCTCACAGAGGA A AAAGTTGCACATTGCTCACTCTGCCTCCACGCTGGATGAGGCCTGCCGAGGAGGAGGAGGAGGAGGAGGCCTGCCGAGGAGGAGGCCTGCCGAGGAGGAGGCCTGCCGGCTACCGCTACCAGGAGGAGGCCCCCCCC

Gene Expression

0-956-157-395	Query Match 73.2%; Score 966.8; DB 21; Length 1948; Best Local Similarity 86.6%; Pred. No. 3.46-285; Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;	69 TGCGCTGGAGGTATTTGACCGCCTAGGCATGÀTCTACACCGTGGGATACTCCATGTCTCT 128	129 GGCCTCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGGC 188	189 CAACTACATCCACATGCACATGTTCCTGTTTATGCTGCGCGCGC	249 GAAGGACGCTGTGCTCTACTCTGGCTTGACGCTGGATGAGGCCGAGCGCCTCACAGGA 308	309 AGAGTIGCACATCATCGCGAGGTGCCACCTCCGCCGGCGCTGCCGCTAGGCTACGC 368	369 TGGCTGCGCGTGGCGGGGGGCCTTCTTCTTCTTCTGGTACTACTACTACTACTGGAT 428	429 CCTGGTGGAGGGCTGTACTTGCACAGCCTCATCTTCATGGCCTTTTTCTCAGAGAAAA 488	489 GTACCTGTGGGGGTTCACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTG 548	549 GGTCGGTGTCAGAACCTTGGCCAACACTGGGTGCTGGGATCTGAGCTCCGGGCACAA 608	609 GAAGIGGAICATCCAGGIGCCCAICCTGGCAICTGGTGGTGCACATCAICCTTTTTAI 668 1105 AAAGIGGAICAICCAGGIGCCCAICCTGGCCTCCAITGIGCTCAACTTCAICCTCTTCAI 1164	669 CAACATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATGCGGGCCGGTGTGACAC 728	729 CAGGCAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTGGTGT 788	789 GCACTACACCGTCTTCATGGCCTTGCCGTACACCGAGGTCTCAGGGACATTGTGGCAGAT 848	849 CCAGATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTGTTGCCATCATATA 908	909 CTGTTTCTGCAATGGTGAGGCAGAGATTAGGAAGTCATGGAGCCGCTGGACACT 968	969 GGCGTTGGACTTCAAGGCACAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAAT 1028 	1029 GGTGTCTCACACGGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCCTCCCCCTCAG 1088
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Db 985 GTACCTGTGGGGCTTCACAGTCTTCGGCTGGGGTCTGCCCGCTGTCTTCGTGGCTGTGTG 1044	Oy 549 GGTCGGTGTCAGAGCAACCTTGGCCAACACTGGGGTGCTGGGGTCCGGGCACAA 608 Db 1045 GGTCAGTGTCAGAGCTAGGCCAACACCGGGTGCTGGGGATCTCGGGAACAA 1104	Qy 609 GAAGTGGATCATCCAGGTGCCCATCCTGGCATCTGTGCTCAACTTCATCCTTTTAT 668	Qy 669 CARCATCATCCGGGGGCGGTGCTTGCCACTAAGCTTCGGGGGCCGGTGTGGCCG 728 D 1165 CANTATCGTCCGGGTGCTCGCCACCACCAGGGGGGGGGCCGGTGTGACAC 1224	Oy 729 CAGGCAGCAGTACCGGAAGCTGCTCAGGTCCCGTTGGTGCTCGTCGTCTTTTGGTGT 788	Oy 789 GCACTACACCGTCTTCATGGCCGTACACCGAGGTCTCAGGGACATTGTGGCGAGAT 848	OY 849 CCAGATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTGTGCCATCATGA 908	OY 909 CTGTTTCTGCAATGGTGAGGGAGGAGATTAGGAAGTCATGGAGCGGTGGACACT 968	QY 969 GGCGTTGGACTTCAAGCGCAAAGCACGAAGTGGGAGTAGGCTACAGCTATGGCCCAAT 1028 D 1465 GGCACTGGACTTCAAGCGAAGGCACGCAGCAGCAGCAACAGCTATAGCTACAGCCCAT 1524	OY 1029 GGTGTCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCCTCCCCCTCAG 1088	Oy 1089 CCCCGGCCTGCCTCCTGCCACTACCAATGGCCACTCCCAGCTGCCATGCCAA 1145	Oy 1146 GCCAGGGGCTCCAGCCACTGAGACTGAAACCCTACCAGTCACTATGGGGTTCCCAA 1202 Db 1645 GCCAGGGACCCCTGAGACCCTGGAGACCTGCCACCTGCCATGGCTGCTCCCAA 1704	OY 1203 GGACGATGCATTAACGGCTCCTGCTCAGGCCTGGATGAGGAGGCCTCCGGGTCTGC 1262	OY 1263 GCGGCCGCCTCCATTGTTGCAGGAAGGATGGGAAACAGTCATGTGACTGGGCACTAGG 1320	RESULT 8 US-10-956-157-395	; Sequence 395, Application US/10956157 ; Publication No. US20050118625A1 ; GENERAL INFORMATION: ; APPLICANT: Wyeth	SSOCIATED	; CURKENT FILING DATE: US/10/956,15/; CURRENT FILING DATE: 2004-10-04; NUMBER OF SEQ ID NOS: 319805; SOFTWARE: Patentin version 3.2	; SEQ ID NO 395 ; LENGTH: 1948 ; TYPE: DNA ; ORGANISM: Homo sapiens

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             GGTCGGTGTCAGAGCAACCTTGGCCAACACTGGGTGCTGGGATCTGAGCTCCGGGCACAA
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APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Duppner, Harald
APPLICANT: Ports, Jr., John T.
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
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; Publication No. US20040253606A1
; GENERAL INFORMATION:
    APPLICANT: Aziz, Natasha
    APPLICANT: Aziz, Natasha
    APPLICANT: Albert
    TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
    TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
    FILE REFERENCE: 05882.0193.NUUS01
    CURRENT FILING DATE: 2003-11-26
    PRIOR PILING DATE: 2003-11-26
    NUMBER OF SEQ ID NOS: 8393
    SOFTWARE: PatentIn version 3.2
    IENGTH: 2282
                              CCCCCGCCTACTGCCACTGCCACCACCACCACCACCCTCAGCTGCCTGGCCATGCCAA 1644
                                                                                            GCCAGGGACCCCAGGCCCTGGAGACCCTCGACACACCACCTGCCATGGCTGCTCCCAA 1704
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Pred. No. 3.6e-285;
0; Mismatches 162;
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ilarity 86.6%;
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DCATION: (2172)..(2279)
OTHER INFORMATION: n is a,
US-10-723-660-5567
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ORGANISM: Homo sapiens
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Matches 1090; Conserv
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Sequence 1005, Application US/10723860

Publication No. US20040253606A1

Sequence 1005, Application US/10723860

Publication No. US20040253606A1

APPLICANT: Alexia Natasha

APPLICANT: Zlotnik Albert

TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

FILE REPERENCE: 05882.0133 NPUS01

CURRENT APPLICATION NUMBER: 001-11-26

PRIOR FILING DATE: 2003-11-26

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: PatentIn version 3.2
     CCAGATGCACTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTGTCGCAATCATATA 1403
                                                                                                                          GGCGTTGGACTTCAAGCGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAAT 1028
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                                                                                GGTGTCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCCTCCCCCTCAG
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                                                          CTGTTTCTGCAATGGTGAGGTGCAGGCAGAGATTAGGAAGTCATGGAGCCGCTGGACACT
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Pred. No. 1.1e-284;
0; Mismatches 163;
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Best Local Similarity 86.6%;
Matches 1089; Conservative
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; ORGANISM: Homo
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LENGTH: 2171
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                                                                                                                                                                                                                                                                              73.1%; Score 965.2; DB 16; Length
86.6%; Pred. No. 1.1e-284;
tive 0; Mismatches 163; Indels
FILE REPERENCE: 00786/071005
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT FILING DATE: 2003-01-27
FRIOR APPLICATION NUMBER: US 08/471,494
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4.0
                                                                                                                                                                                                                                                                                                  Best Local Similarity 86.6
Matches 1089; Conservative
                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (28)...(1806)
US-10-267-730-4
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; GENERAL INFORMATION:
    APPLICANT: Liaw, Chen W.
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Pred. No. 5.2e-283;
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ORGANISM: Homo sapiens
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Sequence 562, Application US/10925095
Sequence 562, Application US/10925095
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Lia, I-Lin
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Know;
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REPRENCE: AREN 207
CURRENT APPLICATION NUMBER: US/10/925,095
CURRENT APPLICATION NUMBER: US/09/826,509
PRIOR PILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ 1D NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ 1D NO 562
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Pred. No. 5.2e-283;
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ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Castleberry, Tessa A.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Lu, Bihong
APPLICANT: Cwen, Thomas A.
APPLICANT: Smock, Steven L.
TITILE OF INVENTION: Cannine Parathyroid Hormone 1 Receptor FILE REBERENCE: PCICL0891AGER;
CURRENT FILIG DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/229,170
PRIOR PLILIG DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 12
NUMBER OF SEQ ID NOS: 12
SOGTWARE: Patentin version 3.1
SEQ ID NO :
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; ORGANISM: Canine
US-09-943-446-1
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Pred. No. 1.4e-282;
0; Mismatches 158;
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| Sequence 14, Application US/10505486
| Publication No. US20050118639A1
| GENERAL INFORMATION:
| APPLICANT: Takeda Chemical Industries, Ltd.
| TITLE OF INVENTION: Determination of a ligand
| FILE PERERNCE: PO3-0006PCT
| CURRENT APPLICATION NUMBER: US/10/505,486
| CURRENT FILING DATE: 2004-08-20
| PRIOR FILING DATE: 2002-02-22
| PRIOR FILING DATE: 2002-07-23
| PRIOR FILING DATE: 2002-07-23
| PRIOR APPLICATION NUMBER: JP 2002-213949
| PRIOR PILING DATE: 2002-07-23
| PRIOR FILING DATE: 2002-07-23
| PRIOR FILING DATE: 2002-07-23
| PRIOR FILING DATE: 2002-07-23
| ENGRHANDER OF EQ ID NOS: 233
| ENGRHANDER OF EQ ID NOS: 233
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Best Local Similarity 86.8%;
Matches 1079; Conservative (
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                                  TGCGCTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCT
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              Gaps
             30;
            Indels
Pred. No. 2.2e-265; ); Mismatches 173;
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ilarity 84.0%;
Conservative
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Title: Perfect score: Sequence:

US-09-869-565-1 1320 1 atgggggccgcccggatcgc.....tcatgtgactgggcactagg 1320

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

.34239544 segs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

gb_est1:.;
gb_est2::;
gb_est4::;
gb_est4::;
gb_est5::;
gb_est5::;
gb_gss1::; EST:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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BC031578	CR595263	AY398834	CB183774	BG972488	BI102266	BX381740	AY398832	CK595861	CK598594	BQ072459	BF789775	CB600301	CA945951	BG970555	AA575668	CB181376	CK231618	CO569702	AA987157	CB203544	CB322650	CK474354	BF780184
BC031578	CR595263	AY398834	CB183774	BG972488	BI102266	BX381740	AY398832	CK595861	CK598594	BQ072459	BF789775	CB600301	CA945951	BG970555	AA575668	CB181376	CK231618	CO569702	AA987157	CB203544	CB322650	CK474354	BF780184
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64.0	63.6	61.9	57.8	55.5	54.1	53.3	51.1	50.1	49.8	49.8	49.2	48.7	47.7	47.1	46.5	45.7	45.1	44.8	44.1	44.1	43.7	43.7	43.0
844.4	839.8	816.8	762.6	732	714.2	703.2	674.8	661.4	657.4	657.4	650	642.6	629.8	622.2	613.8	603	595.8	591.2	581.8	581.6	576.8	576.8	568.2
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ALIGNMENTS

BC031578 Homo sapiens parathyroid hormolymogis 180885), with apparent BC031578 HTC. HTC. Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata;	Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 2090) Strausberg R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Sheamen, C.M., Schuler, G.D., Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uodin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Bouffard, G.G., Blakesley, R.W., Touchman, J. W., Green, E.D., Dickson, M.C., Rodriuski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,	Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 2090) Strausberg,R. Direct Submission Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs.r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc.
RESULT 1 BC031578 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AUTHORS	TITLE JOURNAL PUBNED REFERENCE AUTHORS TITLE JOURNAL REMARK COMMENT

848

1698

1028

896

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Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies,
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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1 (Dases 1 to 2009)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full length cDNA libraries and normalization
Unpublished
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                                                                                                  GGCGTTGGACTTCAAGCGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAAT
                                                                                                                                                        GCACTACACCGTCTTCATGGCCTTGCCGTACACCGAGGTCTCAGGGACATTGTGGCCAGAT
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                                                                     CAGGCAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTGGTGT
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                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: b Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4506270
This clone has the following problem: retained intron.
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                                                          Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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0; Mismatches 156;
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Best Local Similarity 82.3%;
Matches 1035; Conservative
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AY398834 1101 bp DNA linear GSS 15-DEC-2003
Mus musculus PTHR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
CTGTTTCTGCAATGGCGAGGTACAAGCTGAGAATCAAGAAATCTTGGAGCCGCTGGACACT 1769
                                                                                                GGTGTCTCACACGAGTGTGACCAATGTGGCCCCCCGTGCAGGACTCAGCCTCCCCCTCAG 1088
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                GGCGTTGGACTTCAAGCGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Gargill, M.
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larity 68.1%; Pred. No. 1.3e-199;
Conservative 0; Mismatches 394;
                                                                                                                                                                 CCCCCCCCCTCCTCCTCCACTACCAATGGC 1119
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Science 302 (5652), 1960-1963 (2003)
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/db_xref="taxon:10090"
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/locus_tag="HCM0022"
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Mus musculus
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87.4%; Pred. No. 1.5e-205;
ive 0; Mismatches 132;
                                                             /mol_type="mRNA" _r
/db xref="taxon:9606"
/clone="CS0D1069YC10"
/tissue type="Placenta Cot 28"
/plasmid="pCMVSPORT_6"
                                                organism="Homo sapiens"
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Mus musculus (house mouse)

ESM Mus musculus (bouse mouse)

ENGATOGATA, Craniata; Vertebrata; Euteleostomi;

ENGATOGA, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 929)

SS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

CONTEACT: Robert Straubberg, Ph.D.

Email: Gapbs r@mail.nih.gov

Tissue Procurement: Dr. David Rowe and Dr. Mina

CONTA Library Preparation: Invitrogen Corp

CONA Library Preparation: Invitrogen Corp

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM0318 row: d column: 17

High quality sequence start: 2

High quality sequence start: 2

High quality sequence start: 2

Localion/Qualifiers CB183774 929 bp mRNA linear EST 31-JAN-2003 AGENCOURT 11384721 NIH MGC 164 Mus musculus cDNA clone IMAGE:30244792 5', mRNA sequence. 7 144 192 444 132 252 312 372 432 204 264 rrecararcarcececaderececercececececececececececeracecracecrace cesca de contra d CTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCC TCCCTCACGGTGGCTGTGCTCATCCTGGCCTATTTTAGGCGGCTGCACTGCACGCGCAAC TACATCCACATGCACATGTTCCTGTCGTTTATGCTGCGCGCCGCGAGCATCTTCGTGAAG GACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGAGGCGCCTCACAGAGGAGAG TTGCACATCATCGCGCAGGTGCCACCTCCGCCGGCCGCTGCCCGCTAGGCTACGCTGGC Gaps 4; Length 929; Indels /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:30244792" /lab_host="DH10B (phage_resistant)" Score 762.6; DB 6; Pred. No. 1.1e-185; 0; Mismatches 34; g

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Gapa

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ACCCTACCAGTCACTATGGCGGTTCCC-AAGGACGATGGATTCCTTAACGGCTCCTGCTC 1232
/clone lib="NCI CGAP_Kid14"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. |"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 905)

NHH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10967 row: m column: 16

High quality sequence stop: 841.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Machine (1037)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30458988.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

Z rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Scor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                              For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DI069BB05NP1&c=2183.r. Location/Qualifiers
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602885578F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:5040931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="raxon:10090"
/clone="IWAGE:5040931"
/lab_wots="DH10B (T1 phage-resistant)"
/clone lib="WOI CGAP Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCC 132
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 876)
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffery E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyre Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 790.

High quality sequence stop: 790.
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larity 92.4%; Pred. No. 3.5e-173;
Conservative 0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                  BI102266.1 GI:14553159
                                                                                                                                                                                                          5', mRNA sequence.
BI102266
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TGGGCA 902
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249 GAAGGACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGCGCGCCTCACAGAGGA 308
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1 (bases 1 to 1707)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Retriars, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, White, T. White, T. Sninsky, J.J.,

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, This sequence was made by sequencing genomic exons and ordering them based on alignment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      762 GGGCTGCAGGTGGCTGTGACCTTCTTCCTTACTTCCTGGCCACCAACTACTACTGGAT
                                                                                      AY398832 1707 bp DNA linear GSS 15-DEK
Homo sapiens PTHR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
     CGGCCTGCCCCTCAGCCCCCGCCTACTGCCCACTGCCACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.1%; Score 674.8; DB 9;
larity 61.9%; Pred. No. 6e-163;
Conservative 0; Mismatches 469;
                                                                                                                                                                                                                                                                                                                                                                              Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1707
/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="PTHR1"
/locus_tag="HCM0022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  based on alignment.
Location/Qualifiers
                                                                                                                         genomic survey sequence.
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                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                          GCTGCACTGCACGCCAACTACATCCACGTGCACCTGTCCCTGTCCTTTCCATKGCGCGC 974
                                                                                                                                                                                                                                                          293
                                                                                                                                                                                                                                                                                                                         413
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                        CGCGAGCATCTTCGTGAAGGACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCCGA
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                                                                                                                                                       Indels
                                                                                                                    Score 703.2; DB 5;
Pred. No. 2.5e-170;
5; Mismatches 128;
                                                                                                                      53.3%;
85.6%;
                                                                                                                                                       Conservative
                                                                                                                                    Similarity
                                                                                                                    Query Match
Best Local Simi
Matches 810;
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IndelB

Length 1707;

521 188 248

368

761 428 821

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1..808
/organism="Rattus norvegicus"
/wol_type="mRNA"
/db xref="taxon:10116"
/dlone="IMAGE:7133139"
/tissue type="testis, pooled"
/tissue type="testis, pooled"
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/lab_host="NHHOB TonA"
/lab_host="Site_1"
/lab_host="NHHOB TonA"
/lab_host="Testis, Vector: pExpress-1; Site_1: EcoRV;
Site_2: NOT1: RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
5.-pGACTAGTTCTAGATCGCGAGCGCCCCC(T)25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 1.9 kb. This primary library is numalized (non-normalized primary library is NIH MGC 237) and was constructed by Express Genomics
(Frederick, MD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GGCAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGCTGCTGCTGCTCTTTGGTGTCC 360
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                  NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                            CDNA Library Preparation: Express Genomics CDNA Library Preparation: Express Genomics Consortium (LLNL) DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM15036 row: 1 column: 01 Plate: LLAM15036 row: 1 column: 01 High quality sequence stop: 641.
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Pred. No. 1.5e-159;
0; Mismatches 7;
                                                                        Contact: Daniels S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 RM10M07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.1%;
99.0%;
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                  CCACTACATTGTCTTCATGGCCACACCATACACCGAGGTCTCAGGGACGCTCTGGCAAGT 1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1482 CCCCGGCTACTGCCCACTGCCACCACGGCCACCCTCAGCTGCCTGGCCATGCCAA 1541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1542 GCCAGGGACCCCAGCCCTGGAGACCCTCGAGACCACACCACCTGCCATGGCTGCTCCCAA 1601
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                                                                                                                                                                  1122 ACGGCAGCAGTACCGGAAGCTGCTCAAATCCACGCTGGTGCTCATGCCCCTCTTTGGCGT 1181
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GTACCTGTGGGGCTTCACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTGTG 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACTACACCGTCTTCATGGCCTTGCCGTACACCGAGGTCTCAGGGACATTGTGGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTGTTGCCATCATATA
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                                                                                 549 GGTCGGTGTCAGAGCAACCTTGGCCAACACTGGGTGCTGGGATCTGAGCTCCGGGCACAA
                                                                                                                                                                                                                                                                                               CAACATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATGCGGGCCGGTGTGACAC
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AGENCOURT 17840463 NIH MGC 238 Rattus norvegicus cDNA clone IMAGE:7133139 5', mRNA sequence.
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                         616 ATCATCCAGGTGCCCATCCTGGCATCTGTTGTGCTCAACTTCATCCTTTTTATCAACATC
                                                                                                                                                                                                                                                                                                                                              676 ATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATGCGGGCCGGTGTGACCACCAGGCAG
                                                                                                                     1 GAGGGGCTGTACTTGCACAGCCTCATCTTCATGGCCTTTTTTCTCAGAGAAGAAGTACCTG
                                                                                                                                                                                                                                          GTCAGAGCAACCTTGGCCAACACTGGGTGCTGGGATCTGAGCTCCGGGCACAAGAAGTGG
                                                                               GAGGGCTGTACTTGCACAGCCTCATCTTCATGGCCTTTTT
  DB 7;
49.8%; Score 657.4; DB 7;
llarity 99.7%; Pred. No. 1.6e-158;
Conservative 0; Mismatches 1;
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Matches 669; Conserv
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AUTHORS
TITLE
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/lissue_trace.
/lissue_trace.
/lab host="nblos TonA"
/lab host="nblos TonA"
/clone_lib="NIH MGC_238"
/clone_lib="NIH MGC_238"
/note="Organ: testis; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NotI; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
5-pGACTAGTTCTAGATCGCGAGGGCCCC(T) 25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 1.9 kb. This primary library is normalized (non-normalized primary library is NIH MGC_237) and was constructed by Express Genomics
(FrederIck, MD)"
                                                                                                                                     CGTTGGACTTCAAGCGCAAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGG 1030
                                                                                                                                                                                                                     TGTCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGACTCAGCCTCCCCCTCAGCC 1090
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AGENCOURT 17840193 NIH_MGC_238 Rattus norvegicus cDNA clone
AMMACE:7133502 5', mRNA sequence.
                  AGATGCATTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTTTTGTTGCTCATCATATACT 480
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:
http://image.lln.gov
Plate: LiAMIS037 row: o column: 08
High quality sequence stop: 688.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                   GTTTCTGCAATGGTGAGGTGCAGGCAGAGATTAGGAAGTCATGGAGCCGCTGGACCTGG
                                                          GTTTCTGCAATGGTGAGGTGCAGGCAGAGATTAGGAAGTCATGGAGCCGCTGGACACTGG
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|mol_type="mRNN"
|db_xref="taxon:10116"
|clone="IMAGE:7133602"
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CK598594.1 GI:41111717
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CK598594
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TITLE
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AGENCOURT 6838764 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5761637 5', mRNA sequence.
BQ072459.1 GI:19901505
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11H-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                241 ATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATGCGGGCCGGTGTGACACCAGGGG
                                                                                                                                                                                                                                                                                                                                                 CAGIACCGGAAGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTGGTGTCCACTAC
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                                                                                                                                                                                                                                                               361 ACCGTCTTCATGGCCTTGCCGTACACCGAGGTCTCAGGGACATTGTGGCAGATCCAGATG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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1046
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Contact: Straved by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM9811 row: d column: 07
High quality sequence stop: 683.
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/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Kid14"
/note="Organ: Kidney; Vector: DCMV-SPORT6; Site_1: Not1; Site_2: Sall; Clone unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. |"
676 AAAGGCACGCAGCGGGAGCAGCTATAGCTACGGCCCCATGGTGTCCCACACAGTGT
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Pred. No. 1.3e-156;
0; Mismatches 55;
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/strain="FVB/N"
/db_xref="taxon:10090"
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Best Local Similarity 92.2
Matches 719; Conservative
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DEFINITION
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/ db xrefe "taxon:9606"
/ clone = INAGES:561637"
/ lab host="DH108"
/ clone = ID="NIH MGC 122"
/ lone = ID="NIH MGC 122"
/ lone = "Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20.22 week male spleens. Library is oligo-dr primed and directionally clones. Library is oligo-dr primed and directionally clones (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12810 row: j column: 06
High quality sequence start: 3
High quality sequence stop: 682.
Location/Qualifiers
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/organism="Homo sapiens"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
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                    GCCGCTCCACTCCACGCCAACTACATCCACATGCACATGCTTCTTTTTTTGCTG
                                                                                                                      GCCGAGCGCCTCACGGAGGAAGAGTTGCATATCATCGCGCAGGTGCCGCCTCCACCGCC
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                                                 CGCGCCGCGAGCATCTTCGTGAAGGACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAG
                                                                                                      GCCGAGCGCCTCACAGAGGAAGAGTTGCACATCATCGCGCAGGTGCCACCTCCGCCGGCC
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/wol type="mRNA"
/wol type="mRNA"
/wol type="mRNA"
/dev stage="MAGE:7356565"
/dev stage="MADUT"
/dev stage="MADUT"
/lab host="DH10B (Life Technologies)"
/clone lib="NCI_CGAP_FSO"
/clone lib="NCI_CGAP_FSO"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; UI-R-FSO is a cDNA library constructed from Swarm Rat Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)ls tail. The sequence tag for this library is AGCCGCCGAT. The tumor was provided by Dr Jeff Stevens from University of Iowa.
TAG_LIB=UI-R-FSO
TAG_ESD=AGCCGCGAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mial.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through IMAGE (http://image.llnl.gov)

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                             CA945951 T51 bp mRNA linear EST 12-AUG-2004 UI-R-FS0-cgp-m-11-0-UI.81 NCI CGAP_FS0 Rattus norvegicus CDNA clone IMAGE:7356565 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
   Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 751)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                             -GGGCCCCCGTGCAGGACTCAGCCTCCCCCTCAGCCCCCGC 1095
                                                                                   663 GGGCCCCCGTGCAAGAATCAGCCCTTCCCCCTTACCCCCC 703
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97044477
                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
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Best Local Similarity
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                         603
                                                             1056
                                                                                                                                                           RESULT 14
CA945951/c
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KEYWORDS
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MEDLINE
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Mus musculus (house mouse)

Kan musculus (house mouse)

Rukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mus musculus

Rukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.

Rukaryota; Macaroi.nih.gov/.

Ry NIH-Mach thop://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov Green, M.D.

contact: Robert Strausberg, Ph.D.

Fasue Procurement: Jeffrey E. Green, M.D.

contact: Robert Strausberg, Ph.D.

Fasue Procurement: Jeffrey E. Green, M.D.

contact Robert Strausberg, Ph.D.

Fanalis Gapbs-r@mail.nih.gov

close distribution: MGC close distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM10960 row: e column: 20

High quality sequence stop: 741.

High quality sequence stop: 741.
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60288475F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4972795
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746 AGCTGCTCAGGTCCACGTTGGTGCTCGTGCCGCTCTTTGGTGTGCACTACACCGTCTTCA
                                                                                                                                TGGCCTTGCCGTACACCGAGGTCTCAGGGACATTGTGGCAGATCCAGATGCATTATGAGA
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ATGTTCCTGTCGTTTATGCTGCGCGCGCGGGAGCATCTTCGTGAAGGACGCTGTGCTTAC 267
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Site_2: SalI; cloned unidarectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
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47.1%; Score 622.2; DB 4; Length 765;
Best Local Similarity 93.5%; Pred. No. 2e-149;
Matches 715; Conservative 0; Mismatches 43; Indels 7
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                     'mol_type="mRNA"
'strain="FVB/N"
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Search completed: July 4, 2005, 02:48:48 Job time: 4780 secs

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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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protein search, using sw model OM protein

July Run on:

4, 2005, 02:48:53 ; Search time 84 Seconds (without alignments) 2002.866 Million cell updates/sec

Title: Perfect score:

US-09-869-565-2 2283 1 MGAARIAPSLALLLCCPVLS.......EASGSARPPPLLQEGWETVM 435 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seq seq 8 1 1 1 1 1 1 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04: geneseqp2004s:* geneseqp2002s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	no	A mutant	Tethered	Rat bone	Parathyro	Rat bone	Rat bone	Rat Prote	Mouse GPC	Human tet	Human tet	Human tet	Human PTR	Human par	Human Pro	Human PTH	Human GPC	Human sof	Human wil	Human par	Human Par	Non-endog	Human PTH	Human kid	Canine pa	Human kid
-	Description	Aab07529	Aay96983	Aar92277	Aaw73316	Adh61247	Aar27706	Ade83416	Ado29629	Aay96986	Aay96987	Aay96988	Aab71876	Abp81872	Ade83418	Adf70390	Ado29628	Adq18189	Adq76825	Adr47544	Aaw73317	Abb56385	Adh61248	Aar92278	Abg73825	Aar27707
;	QI	AAB07529	AAY96983	AAR92277	AAW73316	ADH61247	AAR27706	ADE83416	AD029629	AAY96986	AAY96987	AAY96988	AAB71876	ABP81872	ADE83418	ADF70390	AD029628	ADQ18189	ADQ76825	ADR47544	AAW73317	ABB56385	ADH61248	AAR92278	ABG73825	AAR27707
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Query	Match	100.0	99.2	96.1	96.1	96.1	. 95.8	95.8	94.0	91.0	91.0	91.0	88.0	88.0	88.0	88.0	. 88.0	88.0	88.0	88.0	87.7	87.7	87.7	85.9	85.7	81.6
	Score	2283	2264.5	2195	2195	2195	2187	2187	2146	2077.5	2077	2076.5	2008	2008	2008	2008	2008	2008	2008	2008	2002	2002	2002	1960	1957	1862.5
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AAR92276 AAW73315	ADC86169 ADC86169 AAY96985 AAY96984 AAR92275	AAW73314 ADH61245 AAR27704 ADQ76835	AAY99630 AAY99600 ADC42305 ADH61059	AAY99601 ADC42307 ADH61061 AAY90231
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ALIGNMENTS

A mutant parathyroid hormone (PTH) receptor designated rdeltaNt. Mutant; parathyroid hormone; PTH; receptor; rdeltaNt; ligand binding domain. 1. .22 /note= "signal peptide" 23. .435 /note= "mature protein" Potts JT; Location/Qualifiers AAB07529 standard; protein; 435 AA 98WO-US027862. 98WO-US027862. Gardella TJ, Kronenberg HM, (first entry) (GEHO) GEN HOSPITAL CORP. WO200040698-A1. 31-DEC-1998; Homo sapiens 31-DEC-1998; 20-OCT-2000 13-JUL-2000 AAB07529; Key Peptide Protein CCCCCXXX1111X88X1X5X8X6X6X6X11114X8XXXX8XCC

New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity. WPI; 2000-465971/40. N-PSDB; AAA58932.

Claim 17; Fig 1; 81pp; English.

The present sequence represents a mutant parathyroid hormone (PTH) receptor, designated realtaNt. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists

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                                                                                                       CTRNYIHWHWFLSFWLRAASIFVKDAVLYSGFTLDEAERLTEEELHIIAQVPPPAAAAV 120
                                                                                                                             GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFV 180
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                                                                         1 MGAARIAPSLALLLCCPVLSSAYALEVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLH 60
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                                                               1 MGAARIAPSLALLLCCPVLSSAYALEVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLH
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                                Length 435;
                                               Indels
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/label= PTH-1_receptor_signal_sequence
                               3; DB 3;
4e-217;
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/label= PTH-1 receptor
/note= "residue 182 to end"
                               100.0%; Score 2283;
100.0%; Pred. No. 4e-
tive 0; Mismatches
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/label= PTH_residues_1-9
and antagonists of PTH receptor activity
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/label= linker
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                                                Conservative
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                                      al Similarity
435; Conserv
                Sequence 435 AA;
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Synthetic.
Chimeric.
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Best Local &
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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 R-ceptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH:P which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
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                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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                                                                                                                                                                                                                                                                                      Jueppner H;
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99WO-US031108
                                                                 98US-0114577P
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                                                                                                                            GARDELLA T J.
KRONENBERG H M.
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N-PSDB; AAA51732.
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JUEPPNER H.
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Recombinant receptor can be produced in vector/host cell systems and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to screen for (ant) agonists and to raise antibodies. Host cells expressing the receptor are used for diagnosis measurement of PTH serum levels. (Updated on 25-MAR-2003 to correct PF field.)
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receptor (AAR92277) is encoded by cDNA clone R15B (AAT15947) isolated from a rat osteosarcoma ROS 17/2.8 cDNA library. The receptor a G-protein linked receptor having 7 transmembrane domains. It induces an increase in intracellular cAMP and calcium upon challenge with PTH or PTHTP.
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                                                                                                                                                                                              Length 591;
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                                                                                                                                                                                                Score 2195; DB 2;
Pred. No. 3.2e-208;
0; Mismatches 0;
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Best Local Similarity 73.6%;
Matches 435; Conservative (
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PTH-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A rat parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              parathyroid hormone receptor - useful for of e.g. hypercalcaemia, hypo-calcaemia, cancer
                                                                                                                                                                                           Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer.
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/label=_Extracellular_region
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212. .221
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/label= Transmembrane_region
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/label= Extracellular_region
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/label= Transmembrane_region
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|abel= Intracellular_region
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/label= Extracellular_region
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|abel= Intracellular_region
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/label= Transmembrane_region
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/label= Intracellular_region
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                                                 AAR92277 standard; protein; 591 AA
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                                                                                                                                                               Rat bone PTH/PTHrP receptor.
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84
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diagnosis and
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18-MAY-1996
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RESULT 5
ADH61247
                                     This sequence represents the rat parathyroid hormone (PTH) receptor R15B, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or oposum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAVLYSGFTLDEAERLTEEELHIIAQVPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                61 NIMESDKGWTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEWDNIVCWPL
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                                                                                                              Schipani
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                                                                                                           Potts JT,
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                        95US-00471494.
                                              91US-00681702.
92US-00864475.
                                                                                                             Juppner H,
                                                                                   (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                       435; Conservative
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                                                                                                             Abou-Samra A,
Kronenberg HM;
                                                             36-APR-1992;
                       06-JUN-1995;
                                                 05-APR-1991;
24-NOV-1998
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The invention relates to parathyroid hormone (PTH) receptor and its corresponding nucleic acid sequence. The parathyroid hormone receptor polypeptides, polynucleotides and antibodies are useful for diagnosing, prognosticating and treating disorders associated with parathyroid hormone receptors, e.g. hypercalcaemia, hyperparathyroidism, osteoporosis, carcinomas of the breast, lung and prostate, epidermoid cancers of the head and neck of the oseophagus, multiple myeloma, or hypocalcaemia. The DNAs and polypeptides are also useful for screening candidate compounds for antagonistic or agonistic effects on parathyroid hormone receptor activity. The compounds are also useful in manufacturing diagnostic agents used as diagnostic tools to diagnose hypercalcaemia and to distinguish between hypercalcaemic conditions. The present sequence is rat bone PTH/PTHYP (PTH-related protein) receptor protein.
                                                                                                                                                                                      osteopathic; Parathyroid hormone receptor; hypercalcaemia;
hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
oesophagus multiple myeloma; hypocalcaemia; cytostatic; rat; PTH; PTHrP;
PTH-related protein; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated DNA encoding parathyroid hormone receptor polypeptides, useful for diagnosing and treating disorders associated with parathyroid
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92US-00864475.
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ADH61247 standard; protein;
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06-APR-1992;
06-JUN-1995;
24-NOV-1998;
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                                                                                                                                                                              181 REVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK 240
                                                                                                                                                                                                                                                   VEGLYLHSLIFWAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK 360
                                                                                                                                                                                                   DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144
                                                                                                                                                                                                               YTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLA 480
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                                                                                                              61 NIMESDKGWTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEWDNIVCWPL 120
                                                                                                                                                  121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRTWANYSECLKFMTNETRE 180
                                                                                                                                                                                                                                         VEGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK 204
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                                                                                                                                                                                                                                                                                                                                                 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG 384
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                                                                            MGAARIAPSLALLICCPVLSSAYALVDADDVFTKEEQIFLIHRAQAQCDKLLKEVIHTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parathyroid hormone; related protein; calcium; antagonist; antibodies;
                                                                                                                                                                   - EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK
                                            Gaps
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                                          Indels 156;
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                          Length 591;
                        Score 2195; DB 8;
Pred. No. 3.2e-208;
0; Mismatches 0;
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                                                            MGAARIAPSLALLLCCPVLSSAYAL
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                        tch 96.1%;
al Similarity 73.6%;
435; Conservative
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        Sequence 591
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16-MAR-1993
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The rat bone parathyroid hormone/parathyroid hormone related protein

(PTH/PTHIRP) receptor protein sequence was deduced from clone R15B obtd.

by screening a rat osteosarcoma (ROS) cell cDNA library to isolate those expressing functionally intact PTH/PTHYP receptor proteins, performed according to Gearing et al., (EMBO J. 8: 3676, 1989), by identifying colonies capable of binding a suitable radio- labelled ligand. The protein may be used in a therapeutic compsn. to inhibit activation of PTH or PTHYP and thus reduce the level of calcium in the blood. Cpds. capable or PTHYP and thus reduce the level of calcium in the blood. Cpds. capable or PTHYP and thus reduce the level of calcium in the blood. Cpds. capable or PTHYP and thus reduce the level of calcium in the blood. Cpds. capable or portein and DNAs homologous to PTH DNA can be identified using the protein as probes. The sequence may be used for the prodn. of antibodies useful for the treatment, classification, prognosis and/or creatment of disorders related to the interaction between a cell receptor and a ligand such as in hypercalcaemia. See also AAR27704-16. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                New DNA encoding parathyroid hormone receptor, DNA and antibodies - for (differential) diagnosis of hypercalcaemia, and diagnosis and treatment of tumours.
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Potts
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Juppner
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Pred. No. 2e-207;
0; Mismatches 1;
Abou-Samra A,
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Best Local Similarity 73.4%;
Matches 434; Conservative (
Kronenberg HM,
                                                                                                            WPI; 1992-366271/44.
N-PSDB; AAQ29606.
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The invention discloses a composition comprising two or more isolated rat or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the sequence acts for this patent did not form part of the printed the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form dart of the printed specification but was obtained.
                                                                                                                                                                                                                                                                                   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
541 APATETETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 591
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Pred. No. 2e-207;
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                                                                                                                                                                                                                                          Protein P25961, SEQ ID NO 11011.
                                                                                                             ADE83416 standard; protein; 591 AA
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                 (first entry)
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(FARB ) BAYER AG.
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Best Local Similarity
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                                                                                                                                                                                                 29-JAN-2004
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                                                                                                                                                                                                                                                                        181 REVPDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMFIMFLSFMLRAASIFVK
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                                                                        1 MGAARIAPSLALLLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA
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 Indels 156; Gaps
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Mismatches
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   434; Conservative
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Sardella TJ, Kronenberg HM,
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KRONENBERG H M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI, 2000-452384/39
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JUEPPNER H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of screening or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; at ranagenic mouse comprising a GPCR gene of the invention; a mouse comprising a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgene or in an endogenous GPCR gene; cells derived from the transgene or in an endogenous GPCR gene; cells derived a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polymucleotides of the invention. The probes which hybridise to GPCR polymucleotides of the invention. The comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, distance); disorders of the adrenal gland; disorders of the colon or intestine or production or and proteine or production. The colon or intestine or production or and production 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., ananama or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NIMESDKGWTPASTSGKPRKEKAPGKFYPESKENKDVPTGSRRRGRPCLPEWDNIVCWPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRTWANYSECLKFMTNETRE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2146; DB 8; Length 591;
Pred. No. 2.3e-203;
                                                                                                                                                                    Hohmann J,
                                                                                                                                                                  IE, Gragerov A, Hohmann J,
Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                              Claim 151; SEQ ID NO 731; 542pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGAARIAPSLALLLCCPVLSSAYAL----
                                                                                                                                                                                                                                                                                                                                         pectoris, Parkinson's disease.
                                                                                                                                                                  3A, Bergmann JE,
Mcilwain KL, Pav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.08;
                                   09-SEP-2003; 2003WO-US028226.
                                                                      09-SEP-2002; 2002US-0409303P,
09-APR-2003; 2003US-0461329P.
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Matches 426; Conservative
                                                                                                                                                                                                                         WPI; 2004-390329/36.
                                                                                                                             (PRIM-) PRIMAL INC.
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13-MAY-2004.
                                                                                                                                                                                        Madisen L,
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301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGMELPAVFVAVWVGVRATLANTGCWDLSSGHKK 360
                                                                                                                                                                                                                                                                                                               264
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                                                                                                                                                                                            145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK 204
                                                                                                                                                                                                                                                                                                                                                                 361 WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 LDFKRKARSGSSSYSYGPMGAHTSVTNVGPRAGLSLPLSPRLLPATTNGHSQLPGHAKPG 540
                                                                                  DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL
                                                                                                                                                                                                                                                                                                            WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parathyroid hormone, conjugate, bone mass, bone reformation, receptor, resorption, remodeling, tether1; osteoporosis, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 APATETETLPVTMAVPKDDGFLNGSCSGLDERASGSARPPPLLQEGWETVM 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 APAIENETIPVTMTVPKDDGFLNGSCSGLDEBASGSARPPPLLQEEWETVM 591
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/label= PTH-1_receptor
/note= "Human PTH-1 receptor residues 182-593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1...23
/label='Signal_sequence
/note= "Human PTH-1 receptor residues 1-23"
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/label= PTH(1-9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33. .36
/label= Linker
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WO200039278-A2
                      Homo sapiens.
                                                                                                              30-DEC-1999;
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                                                                                       06-JUL-2000
                                           Chimeric.
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                                                                                                                                                                               (POTT/)
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                                                                                  Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodelling, treating diseases and disorders associated with decreased tetherl activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKWIIQVPILLASVVLNFILFINIIRVL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHYEM 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKPGAPATET-ETLPVTMAVPKDDGFLN 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNVGPRVGLGLPLSPRLLPTATTNGHPQLPGHAKPGTPALETLETTPPAMAAPKDDGFLN 420
                                                                                                                                                                                                                                                                                                                                                     9
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                    New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                            VLILAYFRRIHCTRNYIHMHMFLSFMLRAASIFVKDAVLYSGFTLDBAERLTEEELHIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSV
                                                                                                                                                                                                                                                                                                                                1 MGAARIAPSLALLLCCPVLSSAYAL-----EVFDRLGMIYTVGYSMSLASLTVA
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                     Length 448;
                                                                                                                                                                                                                                                                                                          26; Indels
                                                                                                                                                                                                                                                                                 91.0%; Score 2077.5; DB 3;
88.8%; Pred. No. 9.8e-197;
iive 11; Mismatches 26; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSCSGLDEEASGSARPPPLLQEGWETVM 435
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                                                                 Example 4; Fig 17; 119pp; English.
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                             Local Similarity
les 398; Conserv
N-PSDB; AAA51735
                                                                                                                                                                                                                                                             Sequence 448 AA;
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Compounds of the structure or formula S-(1) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH). L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 GYAGCRVAVTPFLYFLATNYYMILVBGLYLHSLIFMAFFSEKKYLMGFTVFGWGLPAVFV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 CDTRQQYRKLLKSTLVLMPLFGVHYIVFWATPYTEVSGTLMQVQMHYEMLFNSFQGFFVA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIYCFCNGEVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGTARIAPGLALLICCPVLSSAY--EVFDRLGMIYTVGYSVSLASLTVAVLILAYFRRLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTRNYIHMHMFLSFMLRAASIFVKDAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYAGCRVAVTPFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVWVGVRATLANTGCWDLSSGHKKWIIQVPILASVVLNFILFINIIRVLATKLRETNAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDTRQQYRKLLRSTLVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PTH-1 receptor; resorption; remodeling; tether1; osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 18; 119pp; English
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                                                                                                                                                                                                                                                                                                                                                 99WO-US031108
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N-PSDB; AAA51736.
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Length Indels 47 9 227

240 287 300 347 405

360

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and disorders associated with decreased tetherl activity, increasing CAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTHrP which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                 361 SVTNVGPRVGLGLPLSPRLLPTATTNGHPQLPGHAKPGTPALETLETTPPAMAAPKDDGF 420
                                                                                                                                                                                                                                                                                                                            48 VAVLILAYFRELHCTRNYIHMHMFLSFMLRAASIFVKDAVLYSGFTLDBABRLTEBELHI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, parathyroid hormone/parathyroid hormone-related peptide receptor; PTRR; h15571; immunomodulatory; vascular; hepatic; antiasthma; antiantarondalatory; immunosuppressive; gene therapy; vaccine; G-protein coupled receptor; GFCR; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease; organ-specific autoimmunity; graft rejection; cystic fibrosis.
                                                                                                                                                                                                                                                                         FTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKWIIQVPILASVVLNFILFINIIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIVFGWGLPAVFVAVWVSVRATLANTGCWDLSSGNKKWIIQVPILASIVLNFILFINIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGAARIAPSLALLLCCPVLSSAYAL------EVFDRLGMIYTVGYSMSLASLT
                                                                                                                                                                                                                                                                                                                                                                                                            IAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VLATKLRETNAGRCDTROOYRKLLKSTLVLMPLFGVHYIVFMATPYTEVSGTLMQVQMHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMLFNSFOGFFVAIIYCFCNGEVOAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKPGAPATET-ETLPVTMAVPKDDGF
                                                                                                                                                                3;
                                                                                                                                                              %; Score 2076.5; DB 3;
%; Pred. No. 1.2e-196;
11; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNGSCSGLDEEASGSARPPPLLQEGWETVM 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNGSCSGLDEEASGPERPPALLQEEWETVM 450
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                                                                                                                                                              91.0%;
ilarity 88.4%;
Conservative 11
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29-FEB-2000; 2000US-00515781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                            Query Match
Best Local Similarity
Matches 398; Conserv
                                                                                                                          Sequence 450 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new, S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases
  299 IIYCFCNGEVQAEIKKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRVGLGL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yew compound comprising an amino terminal signaling functional domain
linked to a carboxy-terminal binding portion of parathyroid hormone for
reating mammalian conditions characterized by decreases in bone mass.
                                                               PLSPRILPTATTNGHPQLPGHAKPGTPALETLETTPPAMAAPKDDGFLNGSCSGLDEEAS
                                        PLSPR-LPPATTNGHSQLPGHAKPGAPATET-ETLPVTMAVPKDDGFLNGSCSGLDBEAS
                                                                                                                                                                                                                                                                                                                                                                                                                             PTH; parathyroid hormone; conjugate; bone mass; bone reformation; PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39. .450
/label= PTH-1_receptor
/note= "Human PTH-1 receptor residues 182-593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .23
/label= Signal_sequence
/note= "Human PTH-1 receptor residues 1-23"
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                                                                                                                                                                                                                                                                                                                                                                                       Human tethered PTH-1 receptor, Tether-R11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24. .34
/label= PTH(1-11)
                                                                                                                                                                                                                                                                 AAY96988 standard; protein; 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35. .38
/label= Linker
                                                                                                                        GSARPPPLLQEGWETVM 435
                                                                                                                                                              GPERPPALLOEEWETVM 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gardella TJ, Kronenberg HM,
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                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GARDELLA T J.
KRONENBERG H M.
POTTS J T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA51737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200039278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                               31-OCT-2000
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Key Peptide

AAY96988

Peptide Peptide Protein GARD/) KRON/) (JUEP/)

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The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR designated h15571. h15571 GPCR polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression: Such diseases includes immune; haematological, fibrotic, hepatic and respiratory diseases includes immune; cathma, allergies (e.g. allergic rithinits and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity, graft versus host disease, cystic fibrosis and, in particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies against GPCR and in assays to identify modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR polypeptides
                                                                                                                                       Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.
                                                                                                                                                                                                           Disclosure, Fig 2, 145pp; English.
(MILL-) MILLENNIUM PHARM INC.
                                           Lloyd C,
                                                                                       WPI; 2001-138653/14.
                                              Hodge MR,
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Sequence 593 AA;

26 -EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMPLSFMLRAASIFVK 84

181 REVFDRLGMIYTVGYSVSLASLTVAVLILAYFRRLHCTRNYIHMHLFLSFMLRAVSIFVK 240 361 WIIQVPILASIVLNFILFINIVRVLATKLRETNAGRCDTRQQYRKLLKSTLVEMPLFGVH 420 540 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK 204 WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 264 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVALIYCFCNGEVQAEIRKSWSRWTLA 324 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383 61 SIMESDKGWTSASTSGKPRKDKASGKLYPESEEDKEAPTGSRYRGRPCLPEWDHILCWPL 120 121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180 25 9 DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWII LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRVGLGLPLSPRILLPTATTNGHPQLPGHAKP 26 Gaps GAPATET-ETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPLLLQEGWETVM 435 Indels 158; 88.0%; Score 2008; DB 4; Length 593; 67.3%; Pred. No. 1.1e-189; 56; 10; Mismatches 1 MGAARIAPSLALLLCCPVLSSAYAL-----Best Local Similarity 67.3 Matches 399; Conservative 241 421 56 82 145 205 265 325 481 384 Query Match g g Q g g 셤 à g ò 셤 ò ò ð ò δ ઠે g ò ò

541

Disclosure; Fig 1; 523pp; English.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; Also, canner; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis; allergy; osteoprosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; Human parathyroid hormone receptor 1 protein SEQ ID NO:229. Æ (LIFE-) LIFESPAN BIOSCIENCES INC. ABP81872 standard; protein; 593 19-DEC-2000; 2000US-0257144P. 19-DEC-2001; 2001WO-US050107. (first entry) Roush CL, WPI; 2003-046718/04. N-PSDB; ABZ42719. autoimmune diseases. WO200261087-A2 Homo sapiens. 04-MAR-2003 Burmer GC, 08-AUG-2002 ABP81872; ABP81872

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related disease, immunological-related cell proliferative consensation-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, eg. ALDS, Alzheimer's disease, celecoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obseivity, nature, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis ABP2018, which are used in the exemplification of the present invention

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                                          Indels 158;
                          Length 593;
                                          26;
                       Query Match
88.0%; Score 2008; DB 6;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26;
                                                            MGAARIAPSLALLLCCPVLSSAYAL-----
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allalic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expression and an animal subjected to pain, a method for identifying a polynucleotide or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polynpeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more polynpetides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain in treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene the sequence data for this patent did not form part of the printed specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed specification, which is differentially expressed during pain.
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                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                      Woolf C, D'urso D,
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                                                BAYER AG
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VEGLYLHSLIFMAFFSEKKYLWGFTVFGWGLPAVFVAVWVSVRATLANTGCWDLSSGNKK 360

VEGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK

WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 264

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This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPP, GFPP). The method is useful for the identification of ligands binding to an orphan receptor protein.
                                                              YIVFMATPYTEVSGTLWQVQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIXKSWSRWTLA 480
                                                                                                        LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
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ligand; orphan receptor protein; fusion protein; fluorescent protein; cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP; GFPuv; Enhanced GFP; EGFP; human; PTH-R.
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23-JUL-2002; 2002JP-00213949.
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N-PSDB; ADF70391.
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- protein search, using sw model OM protein Run on:

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US-09-869-565-2 2283 Title: Perfect score:

1 MGAARIAPSLALLLCCPVLS.......BASGSARPPPLLQEGWETVM 435 Sequence:

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513545 segs, 74649064 residues Searched:

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Issued Patents AA:*

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SUMMARIES	QI	US-08-468-249A-20	US-09-631-603-21	US-08-468-249A-21	US-09-826-509-563	US-08-142-439A-6	US-08-142-551B-125	US-08-869-477-6	US-08-468-249A-19	US-08-468-249A-18	US-09-449-632-2	US-09-449-632-4	US-09-449-632-5	US-09-631-603-20	US-09-826-509-565	US-08-468-011A-2	US-09-236-468A-2	PCT-US95-07085-2	US-08-811-519-31	US-09-694-519-4	S-08-811-897A-56	US-09-201-474-56	US-09-694-519-6	US-09-694-519-3	US-09-694-519-8	US-08-112-817C-2	US-09-694-519-5	
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	Length	591	59	59	593	28	28	28	58	51	23	54:	57	55	25	54.	541	54.	207	459	132	1324	44	45	45	45	45	
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	Score	2195	2008	2002	2002	1710	1710	1710	1710	1551	1465	1130	1068	1050.5	1044.5	1036	1036	1036	960.5	176	775.5	775.5	773.5	772	772	762.5	762.5	
	Result No.		7	m	4	C)	9	7	80	0	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23	24	25	56	

28	757.5	33.2	449	н	US-08-142-439A-5	Sequence 5, Appli
29	757.5	33.2	449	7	US-08-869-477-5	Sequence 5, Appli
30	752.5	33.0	457		US-09-631-603-23	Sequence 23, Appl
31	752.5	33.0	457	4	US-09-694-519-1	Sequence 1, Appli
32	747	32.7	440	4	US-09-631-603-22	
33	746.5	32.7	457	4	US-09-826-509-579	Sequence 579, App
34	741	32.5	460	4	US-09-694-519-2	Sequence 2, Appli
35	738	32.3	440	4	US-09-826-509-567	Sequence 567, App
36	718	31.4	447	4	US-09-694-519-9	Sequence 9, Appli
37	687	30.1	448	~	US-08-811-897A-22	Sequence 22, Appl
38	687	30.1	448	~	US-08-855-213-22	
39	. 687	30.1	448	٣	US-09-201-474-22	22,
40	687	30.1	468	4	US-09-631-603-19	19,
41	687	30.1	525	N	US-08-811-897A-23	
42	687	30.1	525	7	US-08-855-213-23	Sequence 23, Appl
43	687	30.1	525	٣	US-09-201-474-23	23,
44	684	30.0	448	7	US-08-811-897A-18	
45	684	30.0	448	~	US-08-855-213-18	Sequence 18, Appl
					AL. LGNMENTS	
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. E. III.	-					

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Sequence 20. Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: BUCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
CITY:
MA

COUNTRY:
USA

ZIP:
COMPUTER:
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TYPE: amino acid
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MOLECULE TYPE: protein
RESULT 1
US-08-468-249A-20
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ï Gaps Score 2195; DB 2; Length 591; Pred. No. 1e-209; 0; Mismatches 0; IndelB 156; Query Match
Best Local Similarity 73.6%;
Matches 435; Conservative

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                                                                                                                                                                                                                        121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE
                                                                                                                                                                                                 26 -EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK
                                                                                                                                                                                                                                                                                         DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL
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Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: FIDENCY COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 21
CORRESSPONDEMES ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Hodge, Clare
APPLICANT: Hodge, Clare
APPLICANT: Lloyd, Clare
APPLICANT: Hodge, Natin R.
TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
FILE REFERENCE: 5800-08-03
FURBERY APPLICATION NUMBER: 05/515,781
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDPKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG
                                         MGAARIAPSLALLLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA
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67.3%; Pred. No. 4.3e-191;
cive 10; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Matches 399;
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APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W
APPLICANT: Liaw, Chen W
APPLICANT: Liaw, Chen W
TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: ARRN-207
CURRENT PELING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                 121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
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                                                                                                                                                                                                                 27; Indels 158;
                                                                                                                                                                                  Length 593;
                                                                                                                                                                               ;; Score 2002; DB 2;
;; Pred. No. 1.7e-190;
10; Mismatches 27;
                                                                                                                                                                                                                                                 1 MGAARIAPSLALLLCCPVLSSAYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 563, Application US/09826509; Patent No. 6806054; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acids
                                                                                                                                                                                  87.7%;
67.1%;
                                                                                                                                                                             Query Match
Best Local Similarity 67.1;
Matches 398; Conservative
                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                  US-08-468-249A-21
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361 WIIQVPILASIVLNFILFINIVRVLATKLRETNAGRCDTRQQYRKLLKSPLVLMPLFGVH 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 LDFKRKARSGSSSYSYGPRVSHTSVTNVGPRVGLGLPLSPRLLPTATTNGHPQLPGHAKP 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VEGLYLHSLIFMAFFSEKKYLWGFTVFGWGLPAVFVAVWVSVRATLANTGCWDLSSGNKK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SIMESDKGWTSASTSCKPRKDKASGKLYPESEEDKEAPTGSRYRGRPCLPEWDHILCWPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK 204
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                                                                                                                                                                                                                                                                                                                                                                                                   1 MGTARIAPGLALLICCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK
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                                                                                                                                                                                                                                                                                        Indels 158;
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APPLICANT: Thorens, Bernard
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
TITLE OF INVENTION: (GLP-1)
                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                            ; Score 2002; DB 4;
; Pred. No. 1.7e-190;
10; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6, Application US/08142439A; Patent No. 5670360
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
SEQ ID NO 563
LENGTH: 593
                                                                                                                                                                                                                                  87.7%;
67.1%;
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                                                                                                                                                                                                                               Query Match
Best Local Similarity 67.1<sup>3</sup>
Matches 398; Conservative
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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CORRESPONDENCE ADDRESS:
                                                                                                              TYPE: PRT
CRGANISM: Homo
US-09-826-509-563
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Query Match
Best Local Similarity 80.29
Matches 333; Conservative
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TOPOLOGY: unknow
                                                                                                           STATE: Virginia COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 PGAPATETETLPVTMAVP--KDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.9%; Score 1710; DB 1; Length 585; 80.2%; Pred. No. 2e-161; Live 27; Mismatches 42; Indels 1:
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Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
ATPLE OF INVENTION: RECOMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24-NOV-93
                                                                               FILING DATE: 4-WOV-93

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92

FILING DATE: 25-WAR-92

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697

FILING DATE: 23-WAR-93

ATTORNEY'AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711

REFERENCE/DOCKET NUMBER: 3756.204-US

TELEPHONE: 212 867 0238

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:

LENGTH: 585 amino acid

TYPE: amino acid
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ORGANISM: Didelphis virginiana
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Matches 333; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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US-08-142-551B-125
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266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQABIRKSWSRWTLAL 325
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                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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80.2%; Pred. No. 2e-161;
iive 27; Mismatches 4;
STREET: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
US-08-142-551B-125
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELING DATE: 14-UTN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-07-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAIS, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCRET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LINGUITH SES amino acids
                                                                                                                                                                  ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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476 DFKRKARSGSSTYSYGPWVSHTSVTWVGPRGGLALSLSPRLAPGAGASANGHHQLPGYVK 535
                                                356 IIQVPILAAIVVNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLKSTLVLMPLFGVHY 415
                                                                                                                                                                                                            326 DFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPP---ATTNGHSQLPGHAK 382
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                                                                                                                  266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGBVQAEIRKSWSRWTLAL
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                                                                                                                                                                                                                                                                                                       383 PGAPATETETLPVTMAVP--KDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 435
                                                                                                                                                                                                                                                                                                                                    536 HG--SISENSLPSSGPEPGTKDDGYLNG--SGLYEPMVGE-QPPPLLEEERETVM 585
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APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: BARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
CITY: Boston.
STREET: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US 07/864,475
APPLICATION NUMBER: US 07/864,475
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,702
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34,819
ep. 00786/071003
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
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amino acid
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Matches 333; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                    Sequence 6, Application US/08869477

Sequence 6, Application US/08869477

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: (GLP-1)

NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: No. 5846747 No. 5846747 Disk of No. 5846747 th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 AVLYSGVSTDEIERITEEELRAFTE--PPPADKA-GFVGCRVAVTVFLYFLTTNYYWILV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 145
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383 PGAPATETETLPVTMAVP -- KDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 435
                        536 HG--SISENSLPSSCPEPGTKDDGYLNG--SGLYEPWVGE-OPPPLLEEERETVM 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,477
                                                                                                                                                                                                                                                                                                                                                                           405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIPECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439
FILING DATE: 24-NOV-93
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-NAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-NAR-93
ATTORNEY/AGENT INPORMATION:
NAME: Harrington, James J.
REFERENCE/DOCKET NUMBER: 3756.204-US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 212 867 0123
TELEBHOME: 212 867 0123
INFORMATION FOR ERG ID NO: 6:
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TYPE: amino acid
STRANDEDNESS: single
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ORGANISM: Di
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                     82
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APPLICANT: Rubin, David A.
APPLICANT: Rubin, David A.
APPLICANT: Rubin, David A.
APPLICANT: Rubin, David A.
FITLE OF INVENTION: PHIR and PTH3R Receptors, Methods and Uses Thereof
FILE REFRENCE: 0609-4740001/SEL/M-G
CURRENT APPLICATION NUMBER: US/09/449,632
CURRENT FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: US 60/110,467
PRIOR PILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 536
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                                                                                        86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV
                                                                                                                                                                 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
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                                                                                                                                                                                                                                                                                                                                                                                         326 DFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.2%; Score 1465; DB 4;
Best Local Similarity 68.8%; Pred. No. 4.3e-137;
Matches 284; Conservative 45; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09449632; Patent No. 6541220; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: zebrafish
US-09-449-632-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-449-632-2
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EGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
                                                                                        EGLYLHSLIFMAFFSEKKYLWGFTLFGWGLPAVFVAVWVTVRATLANTECWDLSSGNKKW
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                                                                                                                                IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY
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                                                                                                                                                                                                                                                                                                                                                                             HG--SISENSLPSSGPEPGTKDDGYLNG--SGLYEPMVGE-QPPPLLEEERETVM 585
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US-08-468-249A-18
Sequence 18, Application US/08468249A
Fatent No. 5886148
GENERAL INFORMATION:
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ROCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%; Score 1551; DB 2; Length 5
86.6%; Pred. No. 1.1e-145;
.ive 18; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN 1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US/0864,475
FILING DATE: 06-APR-1992
RIOR APPLICATION NUMBER: US 07/684,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/681,702
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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Best Local Similarity 86.6%
Matches 291; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-249A-18
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COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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Sequence 710, App Sequence 62, App Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 227, App Sequence 526, App Sequence 524, App Sequence 524, App Sequence 565, App Sequence 109, App Sequence 109, App Sequence 109, App Sequence 6, Appli Sequence 68, Appli Sequence 618, App

4 US-10-267-730-19 4 US-10-267-730-19 5 US-10-22-738-18-22 4 US-10-22-738-18-23 4 US-10-372-095-2 4 US-10-372-095-4 4 US-10-372-095-4 4 US-10-225-567A-227 5 US-10-295-027-526 6 US-10-295-027-526 7 US-10-295-027-526 8 US-10-295-027-526 9 US-10-295-027-526 10S-10-295-027-526 10S-10-295-027-526 10S-10-295-027-526 10S-10-295-027-526 10S-10-295-027-526 10S-10-295-039-6 10S-10-333-4 10S-10-333-8 10S-10-333-8 10S-10-333-3 10S-10-333-3 10S-10-333-3 10S-10-333-3 10S-10-333-3 10S-10-255-567A-469 10S-10-255-567A-469 10S-10-255-567A-469 10S-10-255-567A-469 10S-10-255-567A-469 10S-10-255-567A-469 10S-10-292-798-618 10S-10-292-798-618 10S-10-292-798-618 10S-10-398-455-3

1050.5 1050.5 1050.5 1050.5 1050.5 1044.5 1044.5 10148.5 1036 1036 1038 1038 101.5 775.5 772 772

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July 4, 2005, 06:12:35; Search time 464 Seconds (without alignments) 361.683 Million cell updates/sec
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2283
1 MGAARIAPSLALLLCCPVLS.......EASGSARPPPLLQEGWETVM 435
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MRW PUB_pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 64, App. Sequence 1, Ap Sequence 608, Sequence 65,

Sequence Sequence

ALIGNMENTS

Description Query Match Length

267730 M. Badi I. D HORMONE RECEPTOR AND 27 27 27 28/471,494 Version 4.0	1%; Score 2195; DB 14; 5%; Pred. No. 1.5e-189;	Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps	1 MGAARIAPSLALLLCCPVLSSAYAL25		26 25	
JOC_PUBCOMB. Pep: * 10. PUBCOMB. pep: * 10. PUBCOMB. pep: * 10. PUBCOMB. pep: * 10. NBW PUBCOMB. pep: * 10. NBW PUBCOMB. pep: * 11. NBW PUBCOMB. pep: * 11. NBW PUBCOMB. pep: * 12. NBW PUBCOMB. pep: * 13. NBW PUBCOMB. pep: * 14. NBW PUBCOMB. pep: * 15. NBW PUBCOMB. pep: * 16. PUBCOMB. pep: * 17. NBW PUBCOMB. pep: * 18. NBW PUBCOMB. pep: * 19. NBW PUBCOMB. pep: * 10. NBW PUBCOMB. pep: * 11. NBW PUBCOMB. pep: * 12. NBW PUBCOMB. pep: * 13. NBW PUBCOMB. pep: * 14. NBW PUBCOMB. pep: * 15. NBW PUBCOMB. pep: * 16. NBW PUBCOMB.	Sequence 8, Appli Sequence 9, Appli	-229 Sequence 229, App			US-10-925-095-563 Sequence 563, App US-09-943-446-6 Sequence 6, Appli Oy	

2195 2187 2187 2008 2008 2008 2002 2002 2002

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241 DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 300
                                                       361 WIIQVPILASVVLNPILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 420
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121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRTWANYSECLKFMTNETRE 180
                                                                                                           DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144
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                                      EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK
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APPLICANT: Castleberry, Tessa A.
APPLICANT: Lu, Bihong
APPLICANT: Lu, Bihong
APPLICANT: Cown. Thomas A.
APPLICANT: Smock, Steven L.
TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
TILE REFERENCE: PELIOS DAGR.
CURRENT APPLICATION NUMBER: US/09/943,446
CURRENT FILING DATE: 2001-08-30
PRIOR PILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/229,170
PRIOR PILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 12
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Pred. No. 4.1e-185;
2; Mismatches 7;
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Best Local Similarity 72.1%;
Matches 426; Conservative
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US-09-943-446-8
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                                                                       121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRTWANYSECLKFMTNETRE 180
                                                                                                                                            181 REVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK 240
   NIMESDKGWTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEWDNIVCWPL 120
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Pred. No. 8e-189;
0; Mismatches 1; Indels 15.
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APPLICANT: Lu, Bihong
APPLICANT: Lu, Bihong
APPLICANT: Owen, Thomas A.
APPLICANT: Smock, Steven L.
TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
FILE REFERENCE: PC10891AGPR
CURRENT APPLICATION NUMBER: US/09/943,446
CURRENT PILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/229,170
PRIOR PILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Rattus No. US20020146777Alvegicus
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73.4%;
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Best Local S
Matches 434
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Db 241 DAVLYSGATLDEAERLTEBELRAIAQAPPPPATAAAGYCRVAVTFFLYFLATNYYWIL 300	Oy 145 VEGLYLHSLIFWAFFSEKKYLWGFTIFGWGLPAVFVAVWYGVRATLANTGCWDLSSGHKK 204 	Qy 205 WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 264	Oy 265 YTVFMALPYTEVSGTLWOIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLA 324	Qy 325 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383	Qy 384 GAPATET-ETLEVIMAVPKDDGFLANGSCSGLDEBASGSARPPILQEGWETVM 435	RESULT 5 US-10-225-567A-229 : Sequence 229, Application US/10225567A	Sequence 2.73	
Db 181 REVEDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK 240	OY 85 DAVLYSGFTLDEAERLTEBELHIIAOVPPPPAAANGYAGCRVAVTFFLYFLATNYYWIL 144	Qy 145 VEGLYLHSLIFMAFPSEKKYLWGFTIFGWGLPAVFVAVWCVRATLANTGCWDLSSGHKK 204	Qy 205 WIIQVPIIASVVINFILFINIIRVIATKLRETNAGRCDTRQQYRKLIRSTLVLVPLFGVH 264	OY 265 YTVFMALPYTEVGGTLWQIQMHYEMLFNSFOGFFVAIIYCFCNGEVOAEIRKSWSRWTLA 324	QY 3.25 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG 384 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CY 385 APATETETLPVTWAVPKDDGFLNGSCSGLDEEASGSARPPPLLQBGWETVW 435 Db 541 APAIENETIPVTMTVPKODGFLNGSCSGLDEEASGSARPPPLLQBEWETVW 591	SESULT 4 18-09-1446-9 18-09-1446-9 18-09-1446-9 18-09-1446-9 18-09-1446-9 18-09-1446-9 18-09-1446-9 18-09-1466-9 18-09-14	Qy 85 DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144

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421 YIVFWATPYTEVSGTLWQVQWHYEMLFNSFQGFFVAIIYCFCNGEVQAEIKKSWSRWTLA 480
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                                                                                                                           481 LDFKRKARSGSSSYSYGPWYSHTSVTNVGPRVGLGLPLSPRLLPTATTNGHPQLPGHAKP
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                   265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLA
                                                                                                     LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP
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88.0%; Score 2008; DB 17;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26:
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a ligand
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; Sequence 13, Application US/10505486
; Publication No. US2050118639A1
; GENERAL INFORMATION:
    APPLICANT: Takeda Chemical Industries, Ltd.
    TILE REFERENCE: PO3-0006PCT
    CURRENT APPLICATION NUMBER: US/10/505,486
    CURRENT FILING DATE: 2004-08-20
; RIOR APPLICATION NUMBER: JP 2002-45728
; RIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR APPLICATION NUMBER: JP 2002-298237
; RIOR APPLICATION NUMBER: JP 2002-298237
; RIOR APPLICATION NUMBER: JP 2002-298237
; RIOR APPLICATION NUMBER: JP 2002-298237
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LENGTH: 593
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Publication No. US2004025366A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Joinik, Albert
ITILE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
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301 VEGLYLHSLIFMAFFSEKKYLWGFTVFGWGLPAVFVAVWVSVRATLANTGCWDLSSGNKK 360
                                         WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 264
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Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 1006
LENGTH: 593
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US-10-723-860-1006
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QY 384 GAPATET-ETLPVTWAVPKODGFLNGSCSGLDEBASGSARPPFLLQEGWETVM 435	Sequence 21, Application US/10267730 Sequence 21, Application US/10267730 Publication No. US20030153041A1 GENERAL INFORMATION: APPLICANT: Segre, Gino V. APPLICANT: Abou-Samra, Abdul-Badi APPLICANT: Juppner, Harald APPLICANT: Schipani, Erneatina APPLICANT: Schipani, Erneatina TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME FILE REFERENCE: 00786/071005 CURRENT APPLICATION NUMBER: US/10/267,730 CURRENT FILING DATE: 2003-01-27 PRIOR APPLICATION NUMBER: US 08/471,494 PRIOR APPLICATION NUMBER: US 08/471,494	RE: FastSEQ for Windows Version 4.0 NO 21 H: 593 HSPRT 1SM: Homo sapiens 730-21 atch atch cal Similarity 67.1%; Score 2002; DB 14; Length 593;	Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 1 MGAARIAPSLALLLCCPVLSSAVAL	DB I SIMESDKGWISASAYALVDADDVWITAEEQIFLIDHKAQAQCEKKUKEVLQKFA 80 Qy 26 25 Db 61 SIMESDKGWISASTSGKPRKDKASGKLYPESEEDKEAPTGSRYRGRPCLPEWDHILCWPL 120	26	DB 121 GAPGEVVAPPCPDIIIDENNAGHAIRRCDRASSMEUVFGHNRIMANISECVREINNIRE 100 26 -EVPDRLGMIYTVGYSMSLASLIVAVLILAYPRRLHCTRNYIHMHMFLSFMLRAASIFVK 84 05 161	85 DAVLYSGFTLDEAERLITEELHIIAQVPPPAAAAVGYAGGRVAVTFFLYFLATNYWILL 241 DAVLYSGATLDEAERLITEELHIIAQVPPPAAAAVGYAGGRVAVTFFLYFLATNYWILL 241 DAVLYSGATLDEAERLITEELRAIAQAPPPAAAAGYAGGRVAVTFFLYFLATNYWILL	145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK	205 WIIQVPILASVVLNFILFINIRVLATKLRETNAGRCDTROOYRKLLRSTLVLVPLFGVH 	QY 265 YTVFMALPYTEVSGTLMQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLA 3.24 Dh 4.21 YTUFMATDYTEVSGTLMQVQAFFRMTRMLFNRFOGFPVAIIYCFCNGEVQAETKKSWSRWTLA 4.80	325 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSDPLSPR-LPPATTNGHSQLPGHAKP	384 GAPATET-ETLPVTWAVPKDDGFLNGSCSGLDEBASGSARPPPLLQEGWETVM 435
QY 325 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383 DD 481 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRVGLGLPLSPRLLPTATTNGHPQLPGHAKP 540 QY 384 GAPATET-ETLPVTMAVPKDDGFLAGSCSGLDERASGSARPPPLLQEGWETVM 435 I<	NESULT 8 US-09-563 US-09-563 Sequence 563, Application US/09826509 Sequence 563, Application US/09826509 Sequence 563, Application US20030204073A1 GENERAL INFORMATION: APPLICANT: Liaw, Chen W. APPLICANT: Liaw, Chen W. TITLE OF INVENTION: Drotein-Coupled Receptors TITLE OF INVENTION: Protein-Coupled Receptors TITLE OF INVENTION: Protein-Coupled Receptors CURRENT APPLICATION NUMBER: US/09/826,509 CURRENT APPLICATION NUMBER: US/09/826,509 CURRENT APPLICATION NUMBER: US/0195,747 PRIOR PILING DATE: 2001-04-05 PRIOR PILING DATE: 2000-04-07	PRIOR APPLICATION NUMBER: 09/170,496 PRIOR PILING DATE: 1998-10-13 NUMBER OF SEQ ID NOS: 589 SOFTWARE: Patentin Version 2.1 SEQ ID NO 563 LENGTH: 593 TYPE: PRT ORGANISM: HOMO Sapien8 US-09-826-509-563	Query Match 87.7%; Score 2002; DB 10; Length 593; Best Local Similarity 67.1%; Pred. No. 4.4e-172; Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;	Qy 1 MGAARIAPSIALLLCCPVLSSAYAL	Cy 26 25 Db 61 SIMESDKGWTSASTSGKPRKDKASGKLYPESEEDKEAPTGSRYRGRPCLPEWDHILCWPL 120	Qy 26 25 Db 121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180	Oy 26 -EVPDRIGMIYTVGYSMSLASLTVAVLILAYPRRLHCTRNYIHMMFLSFMLRAASIFVK 84 	OY 85 DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144	Qy 14'S VEGLYLHSLIFWAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK 204	Oy 205 WIIQVPILASVVLAFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 264	Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVALIYCFCNGEVQAEIRKSWSRWTLA 324	Qy 325 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383

541 GTPALETLETTPPAMAAPKDDGFLNGSCSGLDEEASGPERPPALLQEEWETVM 593

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360 WIIQVPILASIVLNFILFINIVRVLATKLRETNAGRCDTRQQYRKLLKSTLVLMPLFGVH 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 REVFDRLGMIYTVGYSVSLASLTVAVLILAYFRRIHCTRNYIHMHLFLSFMLRAVSIFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH
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                                                          APPLICANT: Pfizer Inc.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Lu, Bihong
APPLICANT: Owen, Thomas A.
APPLICANT: Owen, Thomas A.
TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
FILE REFERENCE: PC10891AGPR
CURRENT APPLICATION NUMBER: US 60/943,446
CURRENT FILING DATE: 2001-08-30
PRIOR PILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 6
LENGTH: 595
TYPE: PRT
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.7%; Score 1957; DB 9;
Best Local Similarity 65.6%; Pred. No. 5.2e-168;
Matches 394; Conservative 11; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGAARIAPSLALLLCCPVLSSAYAL-
Sequence 6, Application US/09943446
Patent No. US20020146777A1
                                            GENERAL INFORMATION
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                                                                                                                                                              Constitutively Activated Known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.7%; Score 2002; DB 17; Length 593; 67.1%; Pred. No. 4.4e-172;
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                                                                                                       APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitutively, TITLE OF INVENTION: Protein-Coupled Receptors FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/10/925,095
CURRENT FILING DATE: 2004-08-24
PRIOR APPLICATION NUMBER: US/09/826,509
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
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                     Sequence 563, Application US/10925095 Publication No. US20050019840A1 GENERAL INFORMATION: APPLICANT: Lehmann-Bruinsma, Karin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 67.19
Matches 398; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-925-095-563
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LENGTH: 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 EVFDRLGMIYTVGYSISLGSLTVAVLILGYFRRLHCTRNYIHMHLFVSFMLRAVSIFIKD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPP---ATTNGHSQLPGHAK 382
                                           APPLICANT: Segre, Gino V.
APPLICANT: Segre, Gino V.
APPLICANT: Segre, Gino V.
APPLICANT: Stonenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Object, Jr., John T.
APPLICANT: Schipani, Ernestina
TILLE OF INVENTION: PARATHYROID HORWONE RECEPTOR AND DNA ENCODING SAME
FILE REFERENCE: 00786/071005
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 08/471,494
PRIOR PILING DATE: 1995-66-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 585;
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Sequence 710, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO

APPLICANT: AKIYAMA, YUTAKA

APPLICANT: AKIYAMA, YUTAKA

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REPERRENCE: 084315/0152

CURRENT APPLICATION UNDER: US/10/017,161

CURRENT FILING DATE: 2002-12-18
                                                                                                                                                                                                                                                                                                                                                                                                           74.9%; Score 1710; DB 14;
80.2%; Pred. No. 1.1e-145;
ive 27; Mismatches 42;
; Sequence 19, Application US/10267730; Publication No. US20030153041A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 80.2
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Didelphoidea
                                                                                                                                                                                                                                                                                                                                                                        US-10-267-730-19
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Sequence 622, Application US/10292798
| Publication No. US20030235833A1 |
| GENERAL INFORMATION:
| APPLICANT: SUWA, MAKIKO |
| APPLICANT: ASAI, KIYOSHI |
| APPLICANT: AKIYAWA, YUTAKA |
| APPLICANT: ABURATANI, HIROYUKI |
| APPLICANT: ABURATANI, HIROYUKI |
| TITLE OF INVENTION GUARDER: US/10/292, 798 |
| CURRENT PELICANT: 2002-11-13 |
| PRIOR PILING DATE: 2001-12-18 |
| PRIOR FILING DATE: 2001-017,161 |
| PRIOR FILING DATE: 2001-06-18 |
| NUMBER OF SEQ ID NOS: 2070
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FNSFQVRSAGPGLAEGGRGSGGRPDSRHPSSQGFFVAIIYCFCNGEVQAEIKKSWSRWTL 784
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                                                                                                                                                                                                 Query Match 74.4%; Score 1698; DB 14; Best Local Similarity 59.9%; Pred. No. 2.6e-144; Matches 356; Conservative 11; Mismatches 31;
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    2001/246789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 710
LENGTH: 964
                                                                                                                                     ORGANISM: Homo sapiens
US-10-017-161-710
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                                                                                                                       TYPE: PRT
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Length 515;

ORGANISM: Didelphoidea

US-10-267-730-18

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US-10-267-730-18
; Sequence 18. Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Schipani, Ernestiad
; TITLE OF INVERTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 07086/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFUPARE: FastsEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       557 VAVTFFLYFLATNYYMILVEGLYLHSLIFWAFFSEKKYLMGFTVFGWGLPAVFVAVWWSV
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                                                                                                                                                             Indels 196;
                                                                                                                           Length 964;
                                                                                                                         74.4%; Score 1698; DB 15;
59.9%; Pred. No. 2.6e-144;
iive 11; Mismatches 31;
                                                                                                                                                                                              26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYF----
                                                                                                                      Query Match
Best Local Similarity 59.9%
Matches 356; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                    JS-10-292-798-622
                SEQ ID NO 622
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Job time

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                                                                                                                                                              26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
                                                                                                                                                                                                                     206 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY
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                            Gaps
                          3;
                          Indels
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Query Match 67.9%; Score 1551; DB 14; Best Local Similarity 86.6%; Pred. No. 2.3e-131; Matches 291; Conservative 18; Mismatches 24;
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OM protein - protein search, using sw model

July Run on:

4, 2005, 04:26:48; Search time 24 Seconds (without alignments) 1743.929 Million cell updates/sec

US-09-869-565-2

2283 1 MGAARIAPSLALLLCCPVLS.........BASGSARPPPLLQEGWETVM 435 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	parathyroid hormon			-	_	parathyroid hormon	vasoactive intesti	secretin receptor	secretin receptor	vasoactive intesti	vasoactive intesti	pituitary adenylat	pituitary adenylat	PACAP/VIP receptor	vasoactive intesti	pituitary adenylat		pituitary adenylat	vasoactive intesti	pituitary adenylat	pituitary adenylyl	gastric inhibitory	gastric inhibitory	glucose-dependent	gastric inhibitory	glucagon-like pept	glucose-dependent	qlucadon receptor	1
SUMMARIES	e e	154195	S44203	159297	A49191	A39286	A57519	JH0594	816319	JC2532	JC2194	JC2195	JN0902	JN0616	JU0185	839069	S33449	839061	S36114	G02822	S47631	839060	JC2462	G02234	866676	153273	A46172	137411	J01957	
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,	* Query Match	95.8	94.0	93.5	88.0	74.9	46.0	33.8	33.2	32.6	32.5	32.5	30.1	30.0	29.6	29.5	29.4	29.4	29.4	29.5	29.5	28.8	28.4	27.8	27.8	26.9	26.5	9	26.1	,
	Score	2187	2146	2134	2008	1710	1050.5	772	757.5	745	741	741	687	684	676.5	672.5	671	671	671	999	999	657	649	634.5	634.5	613.5	604	597.5	595.5	Č
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glucagon-like pept	glucagon receptor	glucagon receptor	somatoliberin rece	growth hormone-rel	growth hormone-rel	growth hormone-rel	calcitonin recepto								
184494	JC4363	JC2041	A45363	146586	S29753	S29754	160800	S33746	149154	137217	A37430	S34486	A39285	JC2477	147130
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463 2 3	485 2	477 2	423 2	451 2	423 2	464 2	515 2	479 2	515 2	474 2	478 2	490 2	482 2	461 2	498 2
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592 25.9 463 2 3	25.5 485 2	25.0	24.9	24.9	24.6	23.4	22.8	22.7	22.5	22.4	22.4	21.8	21.4		20.8

ALIGNMENTS

RESULT 1
154195
parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text change 09-Jul-2004
C;Accession: I54195; A42698 _
R; Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
Genomics 20, 20-26, 1994
A, Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (F

A; Reference number: 154195; MUID: 94292182; PMID: 8020952

A;Accession: 154195 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-591 <RES>

Ajcross-references: UNIPROT:P25961; GB:L19475; NID:g467316; PIDN:AA468098.1; PID:g467317
BjAbou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Urer
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
Ajritle: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both cAMP and inositol trisphosphates and increases intracellular free calcium.
Ajritle: Agelerance number: A42698
Ajritle: Agelerance number: A42698
Ajritle: Agelerance number: A42698
Ajritle: Dandolecule trype: DNA
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A;Residues: 1.585,'G',587-591 <ABO>
A;Experimental source: ROS 17/2.8 osteosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:92187)
C;Superfamily: glucagon receptor

Gaps Indels 156; Length 591; Score 2187; DB 2; Pred. No. 3.4e-174; 0; Mismatches 1; Query Match
Best Local Similarity 73.4%;
Matches 434; Conservative

ij

1 MGAARIAPSLALLLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60 1 MGAARIAPSLALLLCCPVLSSAYAL-------8 셤

61 NIMESDKGWTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEWDNIVCWPL 120 26 ઠે g

84 26 -EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK ð

241 DAVLYSGFTLDEAERLTEEELHIIAQVPPPFAAAAVGYAGCRVAVTFFLYFLATNYYWIL 300 85 DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144 엄 ሯ g



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536 HG--SISENSLPSSGPEPGTKDDGYLNG--SGLYEPMVGE-OPPPLLEEERRIVM 585
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: LNA
A;Residues: 1-593 «RES>
A;Cross-references: UNIPROT:Q03431; EMBL:U22409; NID:g897594; PIDN:AAB60657.1; PID:g8975
R;Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V
Embocrinology 132, 2157-2165, 1993
A;Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa
A;Reference number: A49191; MUID:93238641; PMID:8386612
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C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                           A.; Kong, X.F.; Stuhrmann, H.
                                                                                                                                                                                                              parathyroid hormone/PTH-related peptide receptor - human
NyAlternate names: parathyroid hormone/prathyroid hormone/PTH-related peptide receptor
NyAlternate names: parathyroid hormone/prathyroid hormone related peptide receptor
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 19-Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
Cipacession: 13813; A81911; Islands 2, 22940
Cipate: 19-Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
Cipate: 19-Dec-1993 #sequence revision 18-Nov-1994
Eischipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida Klein, A.; Kong, X.F.; Stuhrmann
Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995
A;Title: Pseudohypoparathyroidism type Ib is not caused by mutations in the coding e
A;Reference number: 138139; MUID:95263723; PMID:7745008
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A;Residues: 1753 cSCH.
A;Residues: 1753 cSCH.
A;Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722
A;Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722
A;Cross-reference (NCBIN:130234)
Bur. J. Pharmacol. 246, 149-155, 1993
A;Title: Cloning and functional expression of a human parathyroid hormone receptor.
A;Reference number: 138113; MUID:93387403; PMID:8397094
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C;Genetics:
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A;Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813
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67.3%; Pred. No. 2.8e-159;
ive 10; Mismatches 26;
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submitted to the EMBL Data Library, November 1994
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A;Molecule type: mRNA
A;Residues: 1-593 <LEV>
  09:59:00 2005
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Best Local Similarity
Matches 399; Conserv
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Darathyroid hormone / parathyroid hormone-related peptide - North American opossum C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu. C;Species: 24-Jan-1992 #text_change 09-Jul-2004 C;Accession: A39286 R;Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; Koscience 254, 1024-1026, 1991 A;Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel A;Reference number: A39286; MUID:92054592; PMID:1658941
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-585 <UUE>
A;Residues: 0.00E>
C;Superfamily: glucagon receptor
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein
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80.2%; Pred. No. 1.8e-134;
cive 27; Mismatches 42;
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Matches 333; Conserv
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protein

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A,Accession: S56014
A,Status: preliminary; translation not shown
A,Accession: S56014
A,Status: preliminary; translation not shown
A,Mocession: S56014
A,Status: preliminary; translation not shown
A,Mocession: 1-26 < PBI->
A,Residues: 1-26 < PBI->
A,Cross-references: EMBL:U10635, NID:9505752; PIDN:AAB48185.1; PID:9514311
C,Superfamily: glucagon receptor
C,Superfamily: glucagon receptor
C,Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F;1-30/Domain: signal sequence #status predicted < SIG>
F;31-459/Product: vasoactive intestinal polypeptide receptor #status predicted < TMI>
F;176-195/Domain: transmembrane #status predicted < TMI>
F;256-277/Domain: transmembrane #status predicted < TM3>
F;256-277/Domain: transmembrane #status predicted < TM5>
F;344-363/Domain: transmembrane #status predicted < TM5>
F;344-363/Domain: transmembrane #status predicted < TM6>
F;376-395/Domain: transmembrane #status predicted < TM6>
F;376
Biochem. J. 308, 719-723, 1995
A,Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene
A,Reference number: S56014; MUID:97104266; PMID:8948424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 SVVINFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHYTVFMALPY 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 TEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTL--ALDFKRKA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 YIIGYSLSLASLLVAMAILSLFRKLHCTRNYIHMHLFMSFILRATAVFIKDMALFNSGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 SILVNFVLFICIIRILVQKLRPPDIGKNDS-SPYSRLAKSTLLLIPLFGIHYVMFAFFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---DNFKAQVKAVFELVVGSFQGFVVAILYCFLNGEVQAELRRKWRRWHLQGVLGWSSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 YTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKDAVLYSGFTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.8%; Score 772; DB 2; Length 459; Best Local Similarity 44.8%; Pred. No. 1.7e-56; Matches 147; Conservative 64; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 R---SGSSSYSYGPMVSHTSVTNVGPRA 356
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                     RESULT 6
A57519
parathyroid hormone receptor 2 precursor - human
N;Alternate names: PTH2 receptor
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57519
C;Date: 270, 18-255-18458, 1995
C;Accession: A57519
A;Title: Identification and functional expression of a receptor selectively recognizing
A;Title: Identification and functional expression of a receptor selectively recognizing
A;Reference number: A57519; MUID:95318121; PMID:7797535
A;Title: Identification and functional expression: A57519
A;Status: preliminary; mucleic acid sequence not shown
A;Accession: A57519
A;Status: preliminary; mucleic acid sequence not shown
A;Residues: 1-550 cMSD>
A;Cross-references: UNIPROT:P49190; GB:U25128; NID:g887966; PIDN:AAC50157.1; PID:g887967
C;Genetics:
A;Cross-references: GDB:731977; OMIM:601469
A;Map position: 2433-2433
C;Superfamily: glucagon receptor
C;Keywords: hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 YWILVEGLYLHNLIFVAFFSDTKYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHKKWIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGVHYTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSR 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 RVVHAHIGVKELESL-----IMÓDDÞQNSIEATSVDKSQYIGCKIAVVMFIYFLATNY 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 ATTNGHSQLPGHAKPGAPATETETLP 394
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206

94

363

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A,Accession: S16319
A;Status: preliminary
A;Nolecule type: mRNA
A;Molecule type: mRNA
A;Rossiues: 1-449 (-S18->
A;Cross-references: UNIPROT:P23811; EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57229
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                            Rishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO 0.10, 1655-1641, 1991
A;Title: Molecular cloning and expression of a CDNA encoding the secretin receptor.
A;Reference number: S16319; MUID:91266890; PMID:1646711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
          C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S16319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.2%; Score 757.5; DB 2; ilarity 44.8%; Pred. No. 2.7e-55; Conservative 64; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 154; Conserv
secretin receptor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Residues: 1-459 <ISB.
A,Cross-references: UNIPROT:P30083; GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641
A,Experimental source: lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                          vasoacti
                                                                                                                                                                                              JH0594

Vasoactive intestinal peptide receptor precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C;Accession: JH0594; S56014

R;Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.

Neuron 8, 811-819, 1992

A;Title: Functional expression and tissue distribution of a novel receptor for A;Reference number: JH0594; MUID:92232309; PMID:1314625

A;Accession: JH0594.
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5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2005

protein search, using sw model ı OM protein

July Run on:

4, 2005, 02:53:08; Search time 90 Seconds (without alignments) 2475.049 Million cell updates/sec

US-09-869-565-2 2283

Title: Perfect score:

1 MGAARIAPSLALLLCCPVLS......EASGSARPPPLLQEGWETVM 435 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Beg Beg 08 08 08 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		ption	rattus norv	mus musculu	mus musculu	mus musculu	homo sapien	canis famil	cervus elap		didelphis m			brachydanio	brachydanio	homo sapien	rattus norv		oryctolagus	rattus norv		rana ridibu	rattus norv	sus scrofa	rattus norv	homo sapien	oryctolagus	homo	homo	homo	fugn	melea	fugu rubrip
		Description	P25961	Q80wu8	Q91wv4	P41593	003431	Q9tu31	Q7yri3	P50133	P25107	Q8nhb4	09pvd3	09pvd2	Cdwq60	P49190	P70555	Q91v95	Q9gmd1	Q76n28	P97751	Q9yhc6	P30083	028992	P23811	P32241	046502	P47872	Q6p2m6	Q8iv17	Q8axv4	091085	Q8axv3
SUMMAKIES		ID	PTRR RAT	Q80WU8	Q91WV4	PTRR MOUSE	PTRR HUMAN	Q9TU31	Q7YRI3	PTRR PIG	PTRR_DIDMA	Q8NHB4	Q9PVD3	Q9PVD2	Q9PWB7	PTR2_HUMAN .	PTR2_RAT	PTR2_MOUSE	Q9GMD1	Q76N28	VIPR MOUSE	Q9YHC6	VIPR_RAT	VIPR_PIG	SCRC_RAT	VIPR_HUMAN	SCRC_RABIT	SCRC_HUMAN	Q6P2M6	Q81V17	Q8AXV4	VIPR_MELGA	Q8AXV3
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		Match Length	591	591	591	591	593	595	589	585	585	964	536	542	575	550	546	546	589	147	459	444	459	458	449	457	445	440	457	440	419	457	419
de	Query	Match	95.8	94.4	94.1	94.0	88.0	85.7	84.6	84.3	74.9	74.4	64.2	50.4	47.2	46.0	44.3	44.1	43.4	34.0	34.0	•	33.8	33.4	٠	33.0	32.8	32.7	32.7	32.7	•	31.9	31.9
		Score	2187	2156	2148	2146	2008	1957	1932	1925	1710	1698	1465	1151	1078	1050.5	1011.5	1006.5	991	777	116	773.5	772	762.5	757.5	752.5	749.5	747	746.5	746	743	729	728
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		Q64fl3 oncorhynchu Q6prd2 cavia porce	Q6prd3 cavia porce	Q8bga4 m mus muscu	Q9ptkl xenopus lae	Q6nxj9 mus musculu	Q64f15 oncorhynchu	P41588 mus musculu	Q90y10 rana ridibu	P35000 rattus norv
Q91BG2 VIPR_CARAU	073769 PACR HUMAN	Q64F <u>L</u> 3 Q6PRD2	Q6PRD3	Q8BGA4	Q9PTK1	Q6NXJ9	Q64FL5	VIPS MOUSE	030VI0	VIPS_RAT
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418	465 468	435	437	459	465	468	457	437	455	437
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31.8	30.	29.	29.	29.	29.	29.	29.	29.	29.	29.
725 718	698 687	683 681.5	681.5	680	680	680	619	676.5	674	672.5
33	34 35	36	38	39	40	41	42	43	44	45

ALIGNMENTS

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Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
Schipani B., Urana P., Richards J., Bonventre J.V., Potts J.T. Jr.,
Kronenberg H.M., Segre G.V.,
"Expression cloning of a common receptor for parathyroid hormone and
parathyroid hormone-related peptide from rat osteoblast-like cells: a
single receptor stimulates intracellular accumulation of both cAMP and
inosicol trisphosphates and increases intracellular free calcium.";
Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992). genomes.";
Genomics 20:20-26(1994).
Genomics 20:20-26(1994).

-! FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by g proteins which activate adenyly! cyclase and also a phosphatidylinositol-calcium second messenger system.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SINILARITY: Belongs to the G-protein coupled receptor 2 family. SEQUENCE FROM N.A.
MEDLINES-94292182; PubMed=8020952;
Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F.,
Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;
"Cloning of a parathyroid hormone/parathyroid hormone-related peptide
receptor (FTHR) cDNA from a rat osteosarcoma (UMR 106) cell line:
chromosomal assignment of the gene in the human, mouse, and rat Kattus norvegisus (xet). Eukaryota; Metazos (Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
arathyroid hormone/parathyroid hormone-related peptide represursor (PTH/PTHr receptor) (PTH/PTHrP type I receptor)
Name=Pthr1; Synonyms=Pthr;
Rattus norvegicus (Rat). 591 AA. PRT; STANDARD; SEQUENCE FROM N.A. NCBI_TaxID=10116; RAT RESULT 1 RAT PTRR

EMBL; M77184; AAA41811.1; -. EMBL; L19475; AAA68098.1; -. PIR; I54195; I54195.

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SECURIORIES FROW N.A.

SETRAIN=CSPEL/6; TISSUE=Brain;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Groube L.H., Derga J.G.,

A Latauberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Nillandon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Gareen B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse CDNA sequences:

""" A definitial analysis of more than 15,000 full-length human

""" A moderation and initial analysis of more than 15,000 full-length human
481 LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG
                                                                  LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                    TAS.
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC051981; AAH51981.1; -
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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GO; GO:0004991, F:parathyroid hormone recept
GO; GO:00302022, P:bone mineralization; IMP.
GO; GO:0001501, P:skeletal development; IMP.
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PROSITE; PS00650; G PROTEIN RECEP F2_2; 1.
PROSITE; PS50227; G PROTEIN RECEP F2_3; 1.
PROSITE; PS50261; G PROTEIN RECEP F2_4; 1.
                                                                                                                                                                                                                                                                                                        591
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InterPro; IPR001879; hormn_receptor.
InterPro; IPR002170; Phrmn_receptor.
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 26,
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Pfam; PF02793; HRM; 1.
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Pthr1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 WIIQVPILASVVLNPILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NIMESDKGWTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEWDNIVCWPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLA 324
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                                                                                                                                                                                                                                                                                                   Parathyroid hormone/parathyroid hormone-
related peptide receptor.
Extracellular (Potential).
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                                                                                                                           PRINTS, PRO0249; GPCRSECRETIN.
SMART; SM00008; Hormk; 1.
PROSITE; PS00649; G PROTEIN RECEP F2_1; 1.
PROSITE; PS0050; G PROTEIN RECEP F2_2; 1.
PROSITE; PS50227; G PROTEIN RECEP F2_3; 1.
PROSITE; PS50221; G PROTEIN RECEP F2_4; 1.
G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
SIGNAL
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4 (Potential).
Extracellular (Potential).
5 (Potential).
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7 (Potential).
Cytoplasmic (Potential).
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Cytoplasmic (Potential).
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By similarity.
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N-linked (GlCNAC. .) (I
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2 (Potential).
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Pred. No. 2.
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N-linked (
                        RGD; 3442; Pthr1.
InterPro; IPR000832; GPCR_secretin.
InterPro; IPR001879; hormn_receptor.
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Pfam; PF02793; HRM; 1.
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161
166
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181 REVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMFMFLSFWLRAASIFVK 240
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski MI., Skalska U., Smailus D.E., Schnerch A., Schein J.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NIMESDKGWTPASTSGKPRKEKAPGKFYPESKENKDVPTGSRRRGRPCLPEWDNIVCWPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:9780; Phr1.
GO; GO:0004991; P:parathyroid hormone receptor activity;
GO; GO:001501; P:bone mineralization; IMP.
GO; GO:001501; P:skeletal development; IMP.
Pfam; PF00002; 7tm 2; 1.
Pfam; PF02793; HRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGAARIAPSLALLLCCPVLSSAYAL----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FVB/N; TISSUE=Kidney;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 AA; 66361 MW; 6E29CF63E5BAFEED CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2e-153;
1; Mismatches
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PRINTS; PR00139; PTRHORMONER.
SMART; SM00008; HOTMR; 1.
PROSITE; PS00649; G PROTEIN RECEP F2 1; 1.
PROSITE; PS00650; G PROTEIN RECEP F2 2; 1.
PROSITE; PS50227; G PROTEIN RECEP F2 3; 1.
PROSITE; PS50261; G PROTEIN RECEP F2 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC013446; AAH13446.1;
HSSP; Q03431; 1BL1.
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Matches 427; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 REVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMFMFLSFMLRAASIFVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
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                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NIMESDKGWTPASTSGKPRKEKAPGKFYPESKENKDVPTGSRRGRPCLPEWDNIVCWPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRTWANYSECLKFMTNETRE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 264
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STRAIN=FVB/N; TISSUE=Kidney;
STRAIN=FVB/N; TISSUE=Kidney;
STRAIN=FVB/N; TISSUE=Kidney;
Strausberg R.D.; Peingold E.A.; Grouse L.H., Derge J.G.,
Klausner R.D.; Collins F.S., Wagner L., Shenmen C.M.; Schuler G.D.,
Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.,
Hopkins R.F.; Jordan H., Moore T., Max S. II., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B.; Bonaldo M.F.; Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                   VEGLYLHSLI FMAFFSEKKYLWGFTI FGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK
                                                                                                                                                              Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musin
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                                                                                                                                                              6; Indels 156;
                                                                                         591;
                                                                                         Length
                     C2E6CCAF2ABAFEEF CRC64;
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Last sequence update)
Last annotation update)
                                                                                         DB 2;
                                                                                      Score 2156; DB 2;
Pred. No. 5e-154;
1; Mismatches (
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01-DEC-2001 (TrEMBLrel. 19, Las
01-MAR-2004 (TrEMBLrel. 26, Las
Parathyroid hormone receptor 1.
Name=Pthri;
                     66371 MW;
                                                                                         94.48;
                                                                                                                      al Similarity 72.4
428; Conservative
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                     591 AA;
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                     SEQUENCE
                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c;
MCUaig K.A., Clarke J.C., White J.H.;
McCuaig K.A., Clarke J.C., White J.H.;
Incompose the mouse parathyroid
Incompose Sci. U.S.A. 91:5051-5055(1994).
Incompose This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by groteins which activate adenylyl cyclase and also a phosphatidylinositol-calcium second messenger system.
Is SUBCELLUAR LOCATION: Integral membrane protein.
Is SUBCELLUAR Expression of the G-protein coupled receptor 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C3H/HEHA;
MEDLINE=95034305; PubMed=7524627; DOI=10.1016/0925-4773(94)90093-0;
MEDLINE=95034305; PubMed=7524627; DOI=10.1016/0925-4773(94)90093-0;
Marperien M., van Dijk T.B., Hoeijmakers T., Cremers F.,
Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
"Expression pattern of parathyroid hormone/parathyroid hormone related peptide receptor mRNA in mouse postimplantation embryos indicates involvement in multiple developmental processes.";
Mech. Dev. 47:29-42(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                 PTRR MOUSE STANDARD; Fr., ---
PTRR MOUSE (AC119; Occated) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) 25-OCT-2004 (Rel. 45, Last annotation update) parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTH receptor) (PTH/PTHP type I receptor) Name=Pthr1; Synonyms=Pthr;
                                                                        541 APAIENETIPVTMTVPKDDGFLNGSCSGLDEEASGSARPPFLLQEEWETVM
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MGD; MGI:97801; Pthr1.
G0; G0:0030282; Psbone mineralization; IMP.
G0; G0:001501; P:skeletal development; IMP.
InterPro; IPR000832; GPCR secretin.
InterPro; IPR001879; hormi_receptor.
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PROSITE; PSO0650; G_PROTEIN_RECEP_F2_2; 1.
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L34607; AAA40011.1; JOINED.
L34609; AAA40011.1; JOINED.
L34610; AAA40011.1; JOINED.
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EMBL; L34611; AAA40011.1; -.
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PIR; S44203; S44203.
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(Potential).
(Potential).
                      G_PROTEIN_RECEP_F2_3; 1.
G_PROTEIN_RECEP_F2_4; 1.
receptor; Glycoprotein; Signal; Transmembrane.
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1 (Potential).
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Extracellular (Potential).
3 (Potential).
Gytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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Extracellular (Potential)
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PROSITE; PS50261; G
G-protein coupled re
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TISSUB=Kidney;
MEDLINE=9228611; PubMed=8386612; DOI=10.1210/en.132.5.2157;
Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M., Abou-Samra A.-B., Segre G.V., Jueppner H.;
"Identical complementary deoxyribonucleic acids encode a human renal and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
Endocrinology 132:2157-2165(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95263723; PubMed=7745008; DOI=10.1210/jc.80.5.1611; Schipani B., Weinstein L.S., Bergwitz C., Idda-Klalah A., Kong X.F., Stuhrmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C., Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M., Abou-Samra A.-B., Segre G.V., Jueppner H., "Fseudohypoparathyroidism type Ib is not caused by mutations in the coding exons of the human parathyroid hormone (PTH)/PTH-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93387403; PubMed=8397094; DOI=10.1016/0922-4106(93)90092-N;
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Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
"Binding domain of human parathyroid hormone receptor: from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
25-OCT-2004 (Rel. 45, Last anotation update)
Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTHr receptor)
Name=PTHR1; Synonyms=PTHR;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
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WEDLINE-21918565; PubMed=11850620; DOI=10.1038/ng844;
MEDLINE-21918565; PubMed=11850620; DOI=10.1038/ng844;
HOPPAN S., Gokgoz N., Poon R., Gensure R.C., Yu C., Cole W.G.,
Bell R.S., Jueppner H., Andrulis I.L., Wunder J.S., Alman B.A.;
"A mutant PTH/PTHrP type I receptor in enchondromatosis.";
I.A. Genet. 30:306-310(2002).
I. FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by g proteins which activate adenylyl cyclase and also a phosphatidylinositod.-calcium second messenger system.

C. I. SUBCELLULAR LOCATION: Integral membrane protein.
C. I. TISSUE SPECIFICITY: Expressed in most tissues. Most abundant in Kidney, bone and liver.

C. I. DISEASE: Defects in PTHRI are the cause of Jansen's metaphyseal chondrodysplasia (JMC) [MIN:156400]. JMC is a rare autosomal dominant disorder characterized by a short-limbed dwarfism
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DISEASE: Defects in PTHR1 can be a cause of enchodromatosis [MIN-166000]. Enchondromas are common benign cartilage tumors of bone. They can occur as solitary lesions or as multiple lesions in enchondromatosis (Ollier and Maffucci diseases). Clinical problems caused by enchondromas include skeletal deformity and the potential for malignant change to osteosarcoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Constitutive activation of the cyclic adenosine 3',5'-monophosphate signaling pathway by parathyroid hormone (PTH)/PTH-related peptide receptors mutated at the two loci for Jansen's metaphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION OF VARIANTS JMC ARG-223 AND PRO-410.
MEDLINE-97322091; PubMed=9178745; DOI=10.1210/me.11.7.851;
Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
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DISBASE: Defects in PTHR1 are the cause of chondrodysplasia Blomstrand type (BOCD) [MIM:215045]. BOCD is a severe skeletal
                                                                                                                                                                                                                              MEDLINE=96366745; PubMed=8703170; DOI=10.1056/NEJM199609053351004; Schipani B., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S., Koch S.W., Cole W.G., Jueppner H.; Constitutively activated receptors for parathyroid hormone and parathyroid hormone-related peptide in Jansen's metaphyseal chondrodysplasia."; N. Engl. J. Med. 335:708-714(1996).
Schipani E., Kruse K., Jueppner H.;
"A constitutively active mutant PTH-PTHrP receptor in Jansen-type
metaphyseal chondrodysplasia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99415605; PubMed=10487664; DOI=10.1210/jc.84.9.3052; Schipani E., Langman C.B., Hunzelman J., Le Merrer M., Loke K.Y., Dillon M.J., Sllve C., Jueppner H.; A novel parathyroid hormone (PTH)/PTH-related peptide receptor mutation in Jansen's metaphyseal chondrodysplasia."; J. Clin. Endocrinol. Metab. 84:3052-3057(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98417978; PubMed=9745456; DOI=10.1210/jc.83.9.3373; Zhang P., Jobert A.-S., Couvineau A., Silve C.; "A homozygous inactivating mutation in the parathyroid hormone-/parathyroid hormone-related peptide receptor causing Blometrand chondrodysplasia."; J. Clin. Endocrinol. Metab. 83:3365-3368(1998).
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                                                                                                                                                                                             JMC ARG-223 AND PRO-410.
                                                                                                                     Science 268:98-100(1995)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
GO; GO:0004931; F:parathyroid hormone receptor activity; IEA.
GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
GO; GO:0004991; F:receptor activity; IEA.
InterPro; IPR001873; GPCR secretin.
InterPro; IPR001879; horm_receptor.
InterPro; IPR001170; Phrmn_receptor.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Parathyroid hormone receptor-1.
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PROSITE; PS00649; G PROTEIN RECEP F2 1; 1
PROSITE; PS00650; G PROTEIN RECEP F2 2; 1.
PROSITE; PS5027; G PROTEIN RECEP F2 3; 1.
PROSITE; PS50261; G PROTEIN RECEP F2 3; 1.
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PRINTS; PR00393; PTRHORMONER.
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Pfam; PF02793; HRM; 1.
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TISSUE=Kidney;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SMART; SM00008; HormR; 1
PROSITE; PS00649; G PROTEIN RECEP F2 1; 1.
PROSITE; PS00650; G PROTEIN RECEP F2 2; 1.
PROSITE; PS50227; G-PROTEIN RECEP F2 4; 1.
PROSITE; PS50261; G-PROTEIN RECEP F2 4; 1.
PROSITE; PS50261; G-PROTEIN RECEP F2 4; 1.
3D-structure; Disease mutation; Dwarfism; G-protein coupled receptor; Glycoprotein; Signal; Transmembrane SIGNAL
1 26 Potential.
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related peptide receptor.
Extracellular (Potential).
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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005884; C:integral to plasma membrane; TAS.
GO; GO:0005834; C:inteleus; TAS.
GO; GO:0007187; F:parathyroid hormone receptor activity; TAS.
GO; GO:0007187; F:parathyroid hormone receptor activity; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR001892; GPCR secretin.
InterPro; IPR001899; hormi_receptor.
Pfam; PF002793; HRM, 1.
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EMBL; U22409; AAA50657.1; -
EMBL; U22401; AAB50657.1; -
EMBL; U22401; AAB50657.1; JOINED.
EMBL; U22402; AAB50657.1; JOINED.
EMBL; U22404; AAB50657.1; JOINED.
EMBL; U22404; AAB50657.1; JOINED.
EMBL; U22406; AAB50657.1; JOINED.
EMBL; U22407; AAB50657.1; JOINED.
EMBL; U22407; AAB50657.1; JOINED.
EMBL; U22407; AAB50657.1; JOINED.
EMBL; U17418; AAB50657.1; JOINED.
EMBL; U17418; AAA50774.1; -
PIR; I38139; A49191.
PDB; LETZ; Model; S=168-469.
PDB; LETZ; Model; S=168-469.
GGNEW; U17318; A6161; S=168-469.
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nes 399; Conservative
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MIM; 156400; -.
MIM; 215045; -.
MIM; 166000; -.
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Pfam; PF00002; 7tm 2; 1.
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                                                                                                       61 DIMESDKGWASASTSGKPKKEKASGKLYPESEEDKEVPTGSRHRGRPCLPEWDHILCWPL 120
                                                                                                                                                                                                              DAVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144
                                                                                                                                                                                                                                                       VEGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKK 204
                                                                                                                                                                                                                                                                                                 WIIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVH 264
                                                                                                                                                                                                                                                                                                                                          YTVFMALPYTEVSGTLWQIQMHYEMLPNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLA 324
                                                                                                                                                                                                                                                                                                                                                                                    LDPKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPP-----ATTNGHSQL 377
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                                                                                                                                                                                YIVFWATPYTEVSGTLWQVQMHYENLENSFQGFFVAIIYCFCNGEVQAEIKKSWSRWTLA
                                                         LDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLGLPLSPRLLPAAAATTTATTNGHPPI
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                                                                                                                                                                      - EVPDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVK
                      Gaps
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Parathyroid hormone/parathyroid hormone related protein receptor.
Cervus elaphus (Red deer).
Enkaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
                      Indels 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:membrane; IEA.
GO; GO:0004930; F:G-protein coupled receptor activity; IEA
GO; GO:0004872; F:receptor activity; IEA.
INTERPRO; IPR000832; GPCR secretin.
InterPro; IPR001879; horm_receptor.
Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1957; DB 2;
Pred. No. 4.9e-139;
11; Mismatches 24;
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                                          MGAARIAPSLALLLCCPVLSSAYAL
85.7%;
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           Similarity
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MEDIJIEB-96505358; PubMed=8688470; DOI=10.1016/0167-4781(96)00035-8;
Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
Chandrasekhar S., Hsiung H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 GAPATETETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 435
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Sus.
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2094 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Parathyroid hormone/parathyroid hormone-related
precursor (PTH/PTHr receptor) (PTH/PTHrP type I
Name-PTHR1; Synonyms-PTHR;
Sus scrofa (Pig).
                                                                                                                                        589 AA; 65733 MW; 08A0577FB042A77A
                                                                                                                                                                                         84.6%; Score 1932; DB 2;
65.2%; Pred. No. 3.7e-137;
ive 15; Mismatches 31;
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SMART; SMO0008; HormR; 1.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
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                                                                                                                                                                                                                                                                                                           1 MGAARIAPSLALLLCCPVLSSAYAL-----
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240 148 299 208

88

268 419 479

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                 300 YIHSIIFMAFPSEKKYLWGFTVFGWGLPAIFVAVWVSVRATLANTGCWDLSSGNKKWIIQ 359
                           121 EVVAMPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETREREVF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLALDFK 328
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-!- SUBCELLULAR LOCATION: Integral membrane procein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
                                                                                                                  360 VPILASIVLNFILFINIVRVLATKLRETNAGRCDTRQQYRKLLKSTLVLMPLFGVHYIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 YSGATLDBABRITEBELRAIAQAPLPP-VAATSYVGCRVAVTFFLYFLATNYYWILVEGL
                                                                                                                                                                                                                                                                                                                      149 YLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKWIIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     VPILASVVLNPILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHYTVF
                                                                                    DRIGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKDAVL
                                                                                                                                                                                                      YSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILVEGL
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"A G protein-linked receptor for parathyroid hormone and parathyroid
hormone-related peptide.";
Science 254:1024-1026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schipani E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Didelphis marsupialis virginiana (North American opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MY-1992 (Rel. 22, Created)
01-MOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Parathyroid hormone-parathyroid hormone-related peptide receptor
precursor (PTH/PTHr receptor) (PTH/PTHrP type I receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 TETETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 435
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Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Sch:
Richards J., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     585 AA
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PIR; A39286; A39286.
HSSP; Q03431; 1BL1.
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                                                                              Biochim. Biophys. Acta 1307:339-347(1996).
-!- FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by g proteins which activate adenylyl cyclase and also a phosphatidylinositol-calcium second messenger system (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parathyroid hormone/parathyroid hormone-
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Cytoplasmic (Potential).
By similarity.
By similarity.
N.linked (GICNAC. ..) (Potential).
N.linked (GICNAC. ..) (Potential).
N.linked (GICNAC. ..) (Potential).
                                                                                                                                                                                                                                                             SUBCELLULÂR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000832; GPCR secretin.
InterPro; IPR000832; GPCR secretin.
InterPro; IPR000832; GPCR secretin.
Pfam; PF000793; HRM; 1.
PRINTS; PR00249; GPCRSECREIN.
SMART; SM00069; HORNR; 1.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00277; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS00205; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS002061; G_PROTEIN_RECEP_F2_3; 1.
"Structure and functional expression of a complementary DNA for porcine parathyroid hormone/parathyroid hormone-related peptide
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4 (Potential).
Extracellular (Potential).
5 (Potential).
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Copyright (c) 1993 - 2005 Compugen Ltd.
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435 1 MGAARIAPSLALLLCCPVLS.......BASGSARPPPLLQEGWETVM 435 OLIGO Gapop 60.0 , Gapext 60.0 US-09-869-565-2 Perfect score: Scoring table: Sequence:

2105692 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

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Word size :

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 16Dec04:* 1: geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aab07529 A mutant	Aay96983 Tethered	Aar92277 Rat bone	Aaw73316 Parathyro	Adh61247 Rat bone	Ade83416 Rat Prote	Aay96985 Tethered	Ado29629 Mouse GPC	Aar27706 Rat bone	Aay96984 Tethered	Aay96987 Human tet	Aay96986 Human tet	Aay96988 Human tet	Aaw73317 Human Par	Abb56385 Non-endog	Aab71876 Human PTR	Abp81872 Human par	Human	Adf70390 Human PTH	Adh61248 Human PTH	Ado29628 Human GPC	Adq18189 Human sof	Adq76825 Human wil	Adr47544 Human par	Abg73825 Canine pa
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The present sequence represents a mutant parathyroid hormone (PTH) receptor, designated rdeltaNt. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists

Claim 17; Fig 1; 81pp; English.

> 10 00 0 0 10 10 0 0 0 0 0 10 0 10 10 10	Aav73315 Parathyro Aaw73315 Parathyro Adh61246 Opossum K Aar92278 Human kid Adq76853 Parathyro
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ALIGNMENTS

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New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity.
                                                      A mutant parathyroid hormone (PTH) receptor designated rdeltaNt.
                                                                       Mutant; parathyroid hormone; PTH; receptor; rdeltaNt; ligand binding domain.
                                                                                                                                  1. .22
/note= "signal peptide"
                                                                                                                                                    23. .435 /note= "mature protein"
                                                                                                                                                                                                                                                                              Potts JT;
                                                                                                                        Location/Qualifiers
AAB07529 standard; protein; 435 AA.
                                                                                                                                                                                                                      98WO-US027862.
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                                     20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                               WPI; 2000-465971/40.
N-PSDB; AAA58932.
                                                                                                                                                                                 WO200040698-A1.
                                                                                                       Homo sapiens.
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                   AAB07529;
                                                                                                                          Key
Peptide
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99WO-US031108 98US-0114577P

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30-DEC-1999;
               31-DEC-1998;
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                                                                                                                                GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGMGLPAVFV 180
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                                                                    1 MGAARIAPSLALLLCCPVLSSAYALEVFDRLGMIYTVGYSMSLASLTVAVLLLAYFRRLH
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                                             Gaps
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                               Length 435;
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    .23
    label= PTH-1_receptor_signal_sequence

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                              DB 3;
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/label= PTH-1_receptor
/note= "residue 182 to end"
                                            Mismatches
                              100.0%; Score 435; 1
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/label= PTH_residues_1-9
PTH receptor activity
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/label= linker
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and antagonists of
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435; Conserv
               Sequence 435 AA;
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Chimeric.
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06-JUL-2000

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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tetherl activity, increasing CAMP on ammmalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large native PTH or PTH-P which avoids the need for regular injections to treat osteoporosis
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                                                                                                                                                                                                                                                                                                      New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 TVFWALPYTEVSGTLWQIQMHYEMLFNSFQGFFVALIYCFCNGEVQABIRKSWSRWTLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVFDRIGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BGLYLHSLIFMAFFSEKKYLWGFT1FGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIQVPILLASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVFMALPYTEVSGTLWQ1QMHYEMLFNSPQGFFVAIIYCFCNGEVQAEIRKSWSRWTLAL
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                                                                                                                                                      Jueppner H;
                                                                                                                                                         Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR92277 standard; protein; 591
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Fig 7; 119pp; English
                                                                                                                                                         ĦW,
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                                                                                                                                                         Sardella TJ, Kronenberg
GARDELLA T J.
KRONENBERG H
                                                                                                                                                                                                                    WPI; 2000-452384/39.
N-PSDB; AAA51732.
                                                                                        (JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 410; Conserv
                                                              POTTS J T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 446 AA;
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AAR92277
ID AAR93
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Gaps

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Indels

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301

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82

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361

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481

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421

385

541

Schipani E;

25-MAR-2003 18-MAY-1996

Rattus Key Region Region Region Region

Region Region Region Region Region Region Region Region Region

Region

AAR92277;

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Recombinant receptor can be produced in vector/host cell systems and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to screen for (ant)agonists and to raise antibodies. Host cells expressing the receptor are used for diagnostic measurement of PTH serum levels. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFKRKARSGSSSYSYGPWVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPGA
                                                                                                                                                                                                                                              182 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMIMFLSFMLRAASIFVKD
                                                                                                                                                                                                                                                                                                                242 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYMILV
                                                                                                                                                                                                                                                                                                                                                                                   302 EGLYLASLIFWAFFSEKKYLWGFTIFGWGLPAVFVAVWGVRATLANTGCWDLSSGHKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGBVQABIRKSWSRWTLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFKRKARSGSSSYSYGPWVSHISVINVGPRAGLSLPLPLSPRLPPPATINGHSQLPGHAKPGA
                                                                                                                                                                                                                      26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
                                                                                                                                                                                                                                                                                           86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV
                                                                                                                                                                                                                                                                                                                                                                146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor; PTH receptor; antibody; therapy;
                                                                                                                                              Length
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al Similarity 100.0%; Pred. No. 0;
410; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parathyroid hormone receptor R15B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypercalcaemia, rat.
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N-PSDB; AAV08390.
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                                                                                                                                              Query Match
Best Local Similarity
Matches 410; Conserv
                                                                                                              Sequence 591 AA;
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Kronenberg HM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding vertebrate parathyroid hormone receptor - useful for diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia, cancer
                                                                                                                                         Parathyroid hormone; receptor; parathormone; PTH; parathyroid hormone-related protein; PTHrP; calcium; homeostasis; hypercalcaemia; hypocalcaemia; cancer.
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Abou-Samra A;
                                                                                                                                                                                                                                                                                                                                            212. .221
/label= Intracellular_region
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/label= Transmembrane_region

    192
    label= Extracellular_region

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/label= Extracellular_region
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/label= Extracellular_region
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/label= Transmembrane_region
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/label= Transmembrane_region
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/label= Intracellular_region
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/label= Transmembrane_region
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/label= Intracellular_region
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                                                                                                           Rat bone PTH/PTHrP receptor
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/label= T~
43
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(first entry)
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/label= In
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/label= T
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06-APR-1992; 05-APR-1991;

US5494806-A 27-FEB-1996

Region

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WPI; 2004-051107/05.
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es 410; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 591 AA;
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                                                                                                                           05-APR-1991;
06-APR-1992;
06-JUN-1995;
                                                                                                         09-OCT-2002;
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                                                                                     14-AUG-2003
                                                                                                                                                                                                         Schipani E;
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                                            This sequence represents the rat parathyroid hormone (PTH) receptor R15B, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is eseful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia
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parathyroid hormone receptor - for diagnostic or therapeutic
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                                                                                                                                                                                                                 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV
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                                                                                                                                                         Gaps
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                                                                                                                                      DB 2; Length 591;
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326. .342
/note= "Transmembrane region 4"
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100.0%; Pred. No. v,
... 0; Mismatches
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222. .240
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                           Claim 6; Fig 3; 63pp; English
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                                                                                                                                               al Similarity 100.
410; Conservative
                                                                                                                  Seguence 591 AA;
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Best Local &
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The invention relates to parathyroid hormone (PTH) receptor and its corresponding nucleic acid sequence. The parathyroid hormone receptor polypeptides, polymucleotides and antibodies are useful for diagnosing, prognosticating and treating disorders associated with parathyroid hormone receptors, e.g. hypercalcaemia, hyperparathyroidism, osteoporosis, carcinomas of the breast, lung and prostate, epidermoid cancers of the head and neck of the osophagus, multiple myeloma, or hypocalcaemia. The DNAs and polypeptides are also useful for screening candidate compounds for antagonistic or agonistic effects on parathyroid hormone receptor activity. The compounds are also useful in manufacturing diagnostic agents used as diagnostic tools to diagnose hypercalcaemia and to distinguish between hypercalcaemic conditions. The present sequence is rat bone PTH/PTHFP (PTH-related protein) receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated DNA encoding parathyroid hormone receptor polypeptides, inl for diagnosing and treating disorders associated with parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hormone receptors, e.g. hypercalcemia, osteoporosis or multiple myeloma.
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Conservative 0; Mismatches
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                                   "Transmembrane
                                                                                                   "Transmembrane
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92US-00864475.
95US-00471494.
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Sequence 591 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more isolated rat or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic polynuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynuclectide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that
Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                  386 PATETELPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 435
                                                                     PATETETLPVIMAVPXDDGFLNGSCSGLDEEASGSARPPLLLOEGWETVM 591
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                                                                                                                                                                                                                                                      Rat Protein P25961, SEQ ID NO 11011.
                                                                                                                                                         ADE83416 standard; protein; 591 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                        (first entry)
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                                                                                           26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD 85
                                                                                                                      182 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMEMFLSFMLRAASIFVKD
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Length 591;
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  Score 404; DB 7;
                        100.0%; Pred. No. 0; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tethered PTH-1 receptor, r-del-Nt/Ct.
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92.98;
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                   Best Local Similarity 100.
Matches 404; Conservative
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N-PSDB; AAA51734.
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Synthetic.
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Query Match
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(KRON/)
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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodabling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large mative PTH or PTH-rP which avoids the need for regular injections to treat osteoporosis
linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                          Claim 22; Fig 10; 119pp; English
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Sequence 324 AA;

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   DB 3; Length 324;
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 74.5%; Score 324; DB 3; L6
100.0%; Pred. No. 3.6e-298;
ive 0; Mismatches 0;
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Query Match
Best Local Similarity 100.
Matches 324; Conservative
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G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; intestinal disorder; immune disorder; bone disorder; joint disorder; blood disorder; immune disorder; bone disorder; joint disorder; liver disorder; nutritive disorder; cancer; kidney disorder; liver disorder; puncstate disorder; presst disorder; skin disorder; stomach disorder; pencreas disorder; skin disorder; stomach disorder; pencreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cycostatic; antinflammatory; vasotropic; antianginal; antianrhythmic; CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic; virucide; hepatotropic; antibacterial; antianaemic; antidiabetic;
                                                   AD029629 standard; protein; 591 AA
                                                                                                                                                                                                 Mouse GPCR PTHR1, SEQ ID NO:731.
                                                                                                                                                  (first entry)
                                                                                                                                                  29-JUL-2004
                                                                                                 AD029629;
RESULT 8
                       AD029629
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dermatological; antiulcer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse; Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina Li F; Zeng H; Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, pectoris, Parkinson's disease. 09-SEP-2003; 2003WO-US028226. 09-SEP-2002; 2002US-0409303P-09-SER-2003; 2003US-0461329P-WPI; 2004-390329/36. (PRIM-) PRIMAL INC. murine; receptor N-PSDB; ADO30323 WO20040400000-A2. Mus musculus. 13-MAY-2004

Claim 151; SEQ ID NO 731; 542pp; English.

The invention features to internal and mouse by procedure and nucleic acids encoding them. The invention features to internal to the GPCR proteins and nucleic acids of treating, preventing or diagnosing diseases as sesociated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic moutation in a GPCR agene of the invention, a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived a mutation in a different GPCR polyucleotides of the invention. The curvation in a different GPCR polyucleotides of the invention. The invention is and with comprising a GPCR mucleic acid. The GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR polypeptides and vectors invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR polypeptides and vectors depression, diabetic neuropathy. Parkinson's disease or schizophrenial; disorders of the adrenal gland; disorders (e.g., Alzheimer's disease, Ge.g., andionally and advanced in disorders of the colon or intestine myocardial infarction); muscular disorders (e.g., autoimmune disorders or myocardial infarction); muscular disorders; blood disorders (e.g., autoimmune disorders or this presset) and disorders (e.g., autoimmune disorders (e.g., autoimmune disorders (e.g., autoimmune disorders (e.g., autoimmune disorders (e.g., ansemia or leukaemia); immune disorders (e.g., autoimmune disorders), uterus, prostate, teetis, invention relates to human and mouse G protein-coupled receptors

Sequence 591 AA;

82 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD ; Length 591, 100.0%; Pred. NO. J. Ouery Match Best Local Similarity 100. Matches 318; Conservative 56 ò

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241

86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTPFLYFLATNYYWILV 145

EVFDRIGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD

182

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Gaps

82

145

202

325

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BVFDRLGMIYTVGYSMSLASITVAVLILAYFRRLHCTRNYIHWHWFLSFWLRAASIFVKD 241
                                                                                                                                                                                    302 BGLYLHSLIFWAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW 361
                                                                                                                                                                                                                                                                                         IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY 265
                                                                                                                                                                                                                                                                                                          362 IIQVPILASVVLNPILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY 421
                                                                                                                                                                                                                                                                                                                                                                    DFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPGA 541
                                                                                                                                                                                                                                                                                                                                                                                                               DFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPGA 385
                                                                                                        26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMPLSFMLRAASIFVKD
                                                                                                                                                                     86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV
                                                                                                                                                                                                                                                                                                                                                   266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLAL
                                                                                                                                                                                                                               EGLYLHSLI FMAFFSEKKYLWGFTI FGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
PTH-1 receptor; resorption; remodeling; tether1C; osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 PATETETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPFLLQEGWETVM 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATETETLPVTMAVPKDDGFLNGSCSGLDEBASGSARPPPLLOGGWETVM 591
                                              Length 591;
                                              Score 309; DB 2; Length 59
Pred. No. 1e-283;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .23
/label= PTH-1_receptor_signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37. .335
/label= PTH-1_receptor
/note= "residue 182 to 480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24. 32
/label= PTH_residues_1-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96984 standard; protein; 335 AA.
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                                             / Match 71..0%;
Local Similarity 99.8%;
hes 409; Conservative
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                  Sequence 591 AA;
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Synthetic.
Chimeric.
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                                                Query Match
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Peptide
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(PTH/PTHrP) receptor protein sequence was deduced from clone R15B obtd.

(PTH/PTHrP) receptor protein sequence was deduced from clone R15B obtd.

(By sereening a rat oseeoaarcoma (R0S) cell colmba library to isolate those expressing functionally inteact PTH/PTHrP receptor proteins, performed according to Gearing et al., (RMBO J. 8: 3676, 1989), by identifying according to Gearing et al., (RMBO J. 8: 3676, 1989), by identifying of protein may be used in a therapeutic compan. to inhibit activation of PTH or PTHrP and thus reduce the level of calcium in the blood. Opds. capable of competing with PTH or PTHrP for binding can be identified using the cortein and DNAs homologous to PTH DNA can be identified using fragments of the clone as probes. The sequence may be used for the prodn. of antibodies useful for the treatment, classification, prognosis and/or treatment of disorders related to the interaction between a cell receptor and a ligand such as in hypercalcaemia. See also AAR27704-16. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                  TVFMALPYTEVSGTLWOIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLAL 325
                                                205
                                                                                                        IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY 265
EGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW 361
                                                                                                                                      421
                                                                                                                                                                                    TVFWALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLAL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tew DNA encoding parathyroid hormone receptor, DNA and antibodies - for (differential) diagnosis of hypercalcaemia, and diagnosis and treatment
                                                                                                                          362 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parathyroid hormone; related protein; calcium; antagonist; antibodies;
                                              EGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat bone PTH/PTHrP receptor clone R15B prod
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                                                                                                                                                                                                                                                                                                                                    AAR27706 standard; protein; 591
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                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
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N-PSDB; AAQ29606.
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16-MAR-1993
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Schipani E;
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WO200039278-A2
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                                                                                                         30-DEC-1999;
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                                                                06-JUL-2000
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                                                                                                                                                                                                                                                            JUEP/)
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Matches
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                                                                                                                                                                                                                                                                                                                    Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by inhalation unlike the large mative PTH or PTH-PTP which avoids the need for regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW 205
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                                                                                                                                                                                           New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
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                                                                                    Jueppner H;
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Pred. No. 1.9e-274;
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100.0%; Pred. No. 1...
0; Mismatches
                                                                                    Potts JT,
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                                                                                    Kronenberg HM,
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KRONENBERG H M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                               WPI; 2000-452384/39.
                                          JUEPPNER H.
                                                                                                                                                     N-PSDB; AAA51733
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Synthetic.
Chimeric.
                                                                                  Gardella TJ,
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                        (POTT/)
KRON/)
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Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4); B is a C-terminal binding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the PTH-1 receptor signal sequence; and R is (a portion of PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing cAMP in a mammalian cell having PTH-1 receptors, or screening for a peptide or non-peptide PTH (claimed). The new compound can be administered by regular injections to treat osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .23
/label= Signal sequence
/note= "Human PTH-1 receptor residues 1-23"
24. .32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 49; DB 3; Length 435; 100.0%; Pred. No. 2.4e-37; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      Jueppner H;
                                                                                                                                                                                                                                                                                                                      Potts JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tethered PTH-1 receptor, Tetherl.
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                                                                                                                                                                                                                                                                                                                      Gardella TJ, Kronenberg HM,
99WO-US031108
                                                                        98US-0114577P
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                                                                                                                                         GARDELLA T J.
KRONENBERG H M.
POTTS J T.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-452384/39.
                                                                                                                                                                                                                                                  JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA51736
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RESULT 14
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                                                                                                                                                                                                                                                                                 New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.
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                               37. .448
/label= PTH-1_receptor
/note= "Human_PTH-1_receptor residues 182-593"
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                                                                                                                                                                                                                           Potts JT, Jueppner H;
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                                                                                                                                                                                                                                                                                                                              Example 4; Fig 17; 119pp; English.
(label= PTH(1-9)
          33. .36
/label= Linker
                                                                                                                                                                                                                          Gardella TJ, Kronenberg HM,
                                                                                                                         99WO-US031108
                                                                                                                                              98US-0114577P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000 (first entry)
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                                                                                                                                                                   GARDELLA T J.
KRONENBERG H M.
                                                                                                                                                                                                                                               WPI; 2000-452384/39.
N-PSDB; AAA51735.
                                                                                                                                                                                          (POTT/) POTTS J T. (JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 448 AA;
                                                                            WO200039278-A2.
                                                                                                                                              31-DEC-1998;
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                                                                                                  06-JUL-2000.
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Chimeric.
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                                                                                                                                                                               (KRON/)
(POTT/)
           Peptide
                                Protein
                                                                                                                                                                    (GARD/)
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                                                                                                                                                                                                                  39. .450
/label= PTH-1 receptor
/note= "Human PTH-1 receptor residues 182-593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. .23
/label= Signal_sequence
/note= "Human PTH-1 receptor residues 1-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 450;
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11.3%; Score 49; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 2.5e-37;
Matches 49; Conservative 0; Mismatches 0;
Location/Qualifiers
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                                                                                                            24. .34
/label= PTH(1-11)
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                                                                                                                                                                35. .38
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sardella TJ, Kronenberg HM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GARDELLA T J.
KRONENBERG H M.
POTTS J T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-452384/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUEPPNER H.
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  Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GARD/)
                                                                                                      Peptide
                                                                                                                                                                Peptide
                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUEP/)
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completed: July 4, 2005, 06:28:33
He: 88 secs
                                                                                                              GPCRB.
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Job time
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the human parathyroid hormone (PTH) receptor which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody to parathyroid hormone receptor - for diagnostic or therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
Parathyroid hormone receptor; PTH receptor; antibody; therapy; PTH-related hypercalcaemia; human.
                                                                                                                                                                                                                                                                                                                                                                        Schipani E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSBKKYLWGFT
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Pred. No. 3.2e-37;
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                                                                                                                                                                                                                                                                                                                                                                        Potts JT, Segre GV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%; Scor.
100.0%; Pred. No. s...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Fig 6; 63pp; English
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                                                                                                                                                                                                                                                                                                                           (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Kronenberg HM;
                                                                                                                                                                                                                                                       05-APR-1991;
06-APR-1992;
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                                                                     Homo sapiens
                                                                                                                                                                                                            36-JUN-1995;
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Synthetic.
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                              Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions
                                                                                                                                                                                                                                                                                               The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
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Les 49; Conservative
WPI; 2001-648759/74:
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July 4, 2005, 06:19:15; Search time 28 Seconds (without alignments) 1159.727 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-468-249A-21

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US-08-142-49A-18

US-08-142-49A-19

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US-08-468-249A-19

US-08-468-249A-19

US-08-468-011A-24

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US-09-236-468A-14

US-09-236-468A-14

US-09-236-468A-17

US-09-449-632-2

US-08-468-01A-13

US-08-468-249A-13

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US-08-468-249A-13

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wwwn444wwwwwa444d	T. 1 -468-249A-20 uence 20, Application US/08468249A uence 20, Application US/08468249A MEDLIGANT: Segre et al., Gino V. TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: ADDRESSEE: Fish & Richardson P. STREET: 225 Franklin Street CITY: BOSCON COUNTRY: USA COUNTRY: USA COUNTRY: BOSCON MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: BOSCON COMPUTER: EACHOLIS COMPUTER: BOSCON COMPUTER: BOSCON COMPUTER: BOSCON MEDIUM TYPE: BOSCON COMPUTER: BOSCON COMPUTER: BOSCON COMPUTER: BOSCON COMPUTER: BOSCON COMPUTER: BOSCON SOFTWARE: PATENTION APPLICATION DATA: APPLICATION NUMBER: US 08/468, 2 FILING DATE: 06-APR-1992 RILING DATE: 06-APR-1992 RILING DATE: 06-APR-1991 APPLICATION NUMBER: US 07/681, 7 FILING DATE: 06-APR-1991 APPLICATION NUMBER: US 07/681, 7 RILING DATE: 06-APR-1991 ATTONEY/AGENT INFORMATION: NAME: FRESENCE/DOCKET NUMBER: 07/86/ TELEBCHONE: 617/542-5070 TELEBCANING SEQ ID NO: 20: TELEBCANING SEG ID NO: 20: TELEBCAN	3¢; 0°
0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	T. 1 -468-249A-20 uence 20, Application US/08 werl No. 5886148 APPLICANT: Segre et al., G TITLE OF INVENTION: ENCODI TUTLE OF INVENTION: ENCODI TOTAL SECONDENCES ADDRESS: CORRESPONDENCE ADDRESS: STREET: 225 Franklin Str. STREET: 225 Franklin Str. STRIE: MA COUNTRY: USA CONFUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compation OPERATING SYSTEM: US/0 FILING DATE: 06-APR-1992 RILING DATE: 06-APR-1992 PRILOR APPLICATION DATA: APPLICATION NUMBER: US/0 FILING DATE: 06-APR-1991 REGISTRATION NUMBER: US/0 FILING DATE: 06-APR-1991 APPLICATION NUMBER: US/0 FILING DATE: 06-APR-1991 APPLICATION NUMBER: US/0 FILING DATE: 01-APR-1991 APPLICATION NUMBER: US/0 FILING DATE: 01-APR-1991 APPLICATION NUMBER: US/0 FILING DATE: 01-APR-1991 APPLICATION NUMBER: US/0 TELEBCHOME: FLASACTERISTICS: LERGENAR: 617/542-5070 TELEBCHOR: 591 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: procein -466-249A-20	94 larity 100 Conservative
	cation UG (ON) (ON) (ON) (ON) (ON) (ON) (ON) (ON)	y rvat
	ULT 1 08-468-249A-20 equence 20, Application US GENERAL INFORMATION: APPLICANT: Segre et al. TITLE OF INVENTION: BAR TITLE OF INVENTION: BAR TITLE OF INVENTION: ENC NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Ric STATE: MA COUNTX: USA CONTY: Boston STATE: MA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy d COMPUTER READABLE FORM: MEDIUM TYPE: OF OFF OPERATION S30 PRIOR APPLICATION DATA APPLICATION NUMBER: U FILING DATE: 06-APR-1 PRIOR APPLICATION NUMBER: U FILING DATE: 06-APR-1 REGISTRATION NUMBER: U FILING DATE: 06-APR-1 REGISTRATION NUMBER: U APPLICATION NUMBER: U FILING DATE: 07-ANT-1 REGISTRATION NUMBER: U REGISTRATION NUMBER: U FILING DATE: 07-ANT-1 REGISTRATION NUMBER: U REGISTRATION	Similarity 0; Conser
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                          26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 PATETETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 435
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Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: BNRATHYROLD HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEGURNCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INPORMATION:
NAME: FRASEr, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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COUNTRY: USA
ZIP. 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acid
TYPE: amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-468-249A-21
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Sequence 563, Application US/09826509

Sequence 563, Application US/09826509

Sequence 563, Application US/09826509

Sequence 563, Application US/09826509

GENERAL INFORMATION:

APPLICANT: Linamann-Bruinsma, Karin

TITLE OF INVENTION: NO. 6806054-Endogenous, Constitutively Activated Known G

TITLE OF INVENTION: Protein-Coupled Receptors

FILE REFERENCE: AREN-207

CURRENT APPLICATION NUMBER: US/09/826,509

CURRENT FILING DATE: 2000-04-07

FRIOR FILING DATE: 2000-04-07

FRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589

SOFTWARE PATENTING VARSION 2.1
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APPLICANT: Lloyd, Clare
APPLICANT: Lloyd, Clare
APPLICANT: Lloyd, Clare
APPLICANT: Weich, Nadine
TITLE OF INVENTION: 15571, A No. 6733990e1 GPCR-like Molecule of the
TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
TITLE OF INVENTION: Secretin-Like Pamily and Uses Thereof
TITLE OF INVENTION: Secretin-Like Pamily and Uses Thereof
TITLE OF INVENTION NUMBER: 08/09/631,603
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/146,916
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: PRT
TYPE: 
                                                                                                                     Gaps
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                                                                                                                                                                                                                    121 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 169
                                                                                                                                                                                                                                                                                       277 GYAGCRVAVTFFLYFLATNYYMILVEGLYLHSLIFMAFFSEKKYLMGFT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.3%; Score 49; DB 4; Length 593; Best Local Similarity 100.0%; Pred. No. 4.4e-36; Matches 49; Conservative 0; Mismatches 0; Indels
Query Match 11.3%; Score 49; DB 2; Length 593; Best Local Similarity 100.0%; Pred. No. 4.4e-36; Matches 49; Conservative 0; Mismatches 0; Indels
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11.3%; Score 49; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 4.4e-36;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09631603
Patent No. 6733990
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ORGANISM: Homo sapiens
US-09-826-509-563
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Gaps

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Indels

Length 515;

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Query Match 7.8%; Score 34; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.7e-22; Matches 34; Conservative 0; Mismatches 0;
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                     : 515 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
SEQUENCE CHARACTERISTICS
LENGTH: 515 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                          MOLECULE TYPE: protein US-08-468-249A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 405 Lex
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE ORGANISM: Div
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                        JS-08-142-439A-6
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NUMBER OF SEQ ID NOS: 31

SOFTWARE: 1997-03-04

NUMBER OF SEQ ID NOS: 31

SOFTWARE: 1997-03-04

NUMBER OF SEQ ID NOS: 31

SOFTWARE: 1997-03-04

NUMBER OF SEQ ID NOS: 31

LENGTH: 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 YAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 4; Length 207;
Pred. No. 1.4e-35;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 YAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITI.
STATE: MA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPBY disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
PTLING DATE: 06-01/NN-1995
PTLING DATE: 06-01/NN-1995
PTLING DATE: 06-01/NN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.0%; Score 48; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 48; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00786/071003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-UNN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K. REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-08-811-519-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                            US-08-811-519-31
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TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
TITLE OF INVENTION: (GLP-1)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56703600 No. 5670360disk of No. 5670360th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24.NOV-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.8%; Score 34; DB 1; Le Best Local Similarity 100.0%; Pred. No. 1.9e-22; Matches 34; Conservative 0; Mismatches 0;
                                                 368 NFILFINIIRVLATKLRETNAGRCDTROOYRKLL 401
218 NFILFINIIRVLATKLRETNAGRCDTROOYRKLL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REGISTRATION NUMBER: 38,711
REPERBNCE/DOCKET NUMBER: 3756.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
                                                                                                                                                                                         Sequence 6, Application US/08142439A Patent No. 5670360 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Didelphis virginiana
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORIGINAL SOURCE:
ORGANISM: Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-869-477-6
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                                                                                                                                 AFACTOR OF SOURCE 125

Sequence 125 Application US/08142551B
FREEDER NO. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STREET: US
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor for the Glucagon-Like-Peptide-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-UNN 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-UNN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
PRIOR APPLICATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 30,113
REFERENCE/COMMUNICATION INFORMATION:
TELLEPONE: (415) 854-275
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENDING: TELLEPONE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 NFILFINIIRVLATKLRETNAGRCDTRQQYRKLL 401
   368 NFILFINIIRVLATKLRETNAGRCDTRQQYRKLL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.8%; scc...
100.0%; Pred. No....
0; Mismatches
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COTHER INFORMATION: /note= "PTH receptor"
US-08-142-551B-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-869-477-6

Sequence 6, Application US/08869477

Patent No. 5846747;
GENERAL INFORMATION:
APPLICANT: Thorens, Bernard
ITLE OF INVENTION: Receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
The Additional Similarity 100.0
The Additional State Sta
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TITLE OF INVENTION: (GLP-1)

WUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58467470 No. 5846747disk of No. 584677th America, Inc. STREET: 405 Lexington Avenue, Suite 6400

CITY: New York
STATE: New York
STATE: New York
STATE: 10174-6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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Sequence 19, Application US/08468249A

Patent No. 588614

GENERAL INFORMATION:
TITLE OF INVENTION: PRACHTYROID HORMONE RECEPTOR AND DNA TITLE OF INVENTION: ENCOING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: USA
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 585;
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.8%; Score 34; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.9e-22; Matches 34; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 NFILFINIRVLATKLRETNAGRCDTROOYRKLL 251
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T: Soppet, Daniel R
T: Yi, Li
F: Rosen, Craig A
F: Ruben, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Didelphis virginians
      INFORMATION FOR SEQ ID NO:
                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-24
                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Roseland STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-236-468A-24
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Fatent No. 6030804

GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Soppet, Craig A
APPLICANT: Ruben, Craig A
APPLICANT: Ruben, Serven
TITLE OF INVENTION: G-Procein Parathyroid Hormone receptor
TITLE OF INVENTION: HITDG74
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%; Score 34; DB 2; Length 585; 100.0%; Pred. No. 1.9e-22; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILLIG DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 33,073
TELECHONE: 201-994-1700
TELECHONE: 201-994-1700
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 NFILFINIIRVLATKLRETNAGRCDTRQQYRKLL 251
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                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                               PELLING DATE: 06-JUN-1995
CLASSIFICATION : 530
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,702
PRIOR APPLICATION UNBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 585 amino acids
amino acid
                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roseland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-468-249A-19
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                                              SOFTWARE
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                                               Gaps
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TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
FILE REFERENCE: PP201D1
CURRENT APPLICATION NUMBER: US/09/236,468A
CURRENT FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 08/468,011
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 59
TYPE: PRT
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HLTDG74
Length 59;
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                                            Indels
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APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone rec
TITLE OF INVENTION: HLTDG74
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Garella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
DB 3; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
7.1%; Score 31; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 31; Conservative 0; Mismatches 0;
                                                                                         284 QMHYEMLFNSFQGFFVAIIYCFCNGEVQAEI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 QMHYEMLFNSFQGFFVAIIYCFCNGBVQAEI 314
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                                                                                                                                   8 QMHYEMLFNSFQGFFVAIIYCFCNGEVQAEI 38
  Query Match 7.1%; Score 31; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
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GENERAL INFORMATION:
                                                                                                                                                                                                                             US-09-236-468A-24
Sequence 24, Application US/09236468A
Patent No. 6338951
GENERAL INFORMATION:
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COUNTY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
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; Sequence 2, Application US/09449632
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: User, Harald
; APPLICANT: User, Harald
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609-4740001/SEL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT PILING DATE: 1999-11-30
; PRIOR PILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRI
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| Sequence 14, Application US/09236468A |
| Sequence 14, Application US/09236468A |
| Patent No. 6388B151. |
| GENERAL INFORMATION: G-Fortein Parathyroid Hormone Receptor HLTDG74 |
| TITLE OF INVENTION: G-Fortein Parathyroid Hormone Receptor HLTDG74 |
| FILE REFERENCE: PF201D1 |
| CURRENT APPLICATION NUMBER: US/09/236,468A |
| FILE REPERENCE: 1999-01-25 |
| PRIOR APPLICATION NUMBER: 08/468,011 |
| PRIOR APPLICATION NUMBER: 0
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100.0%; Pred. No. 8.3e-19;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 52;
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FILING DATE: 06-JUN-1>>.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REFISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-994-1740
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TTILE AMINO acids
TELEFAX: 201-994-1744
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ORGANISM: Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-011A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-236-468A-14
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: July 4, 2005, 06:29:11; Search time 80 Seconds (without alignments)
2097.762 Million cell updates/sec
Perfect score: US-09-869-565-2
Sequence: 1 MGARIAPSLALLLCCPVLS......EASGSARPPPLLQEGWETVM 435
Scoring table: OLIGO
Gapop 60.0, Gapext 60.0
Searched: 1722976 seqs, 385795295 residues
Word size: 0
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1722976

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Published Applications AA:*

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15: /cgn2 6/ptodata/2/pubpaa/USO10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Description	Sequence 20, Appl	Sequence 7, Appli	Sequence 8, Appli	Sequence 9, Appli	Sequence 563, App	Sequence 229, App	Sequence 21, Appl	Sequence 1006, Ap	Sequence 563, App	Sequence 13, Appl	Seguence 6, Appli
	1	ID	US-10-267-730-20	US-09-943-446-7	US-09-943-446-8	US-09-943-446-9	US-09-826-509-563	US-10-225-567A-229	US-10-267-730-21	US-10-723-860-1006	US-10-925-095-563	US-10-505-486-13	US-09-943-446-6
		80	14	σ	σ	6	10	14	14	16	17	17	σ
	•	Match Length DB ID	591	591	591	593	593	593	593	593	593	593	595
de	Query	Match	94.3	92.9	73.1	11.3	11.3	11.3	11.3	11.3	11.3	11.3	11.3
		Score	410	404	318	49	49	49	49	49	49	49	49
	Result	Q	1	73	m	4	S	9	7	80	6	10	11

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86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 145

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Sequence 710, App Sequence 622, App Sequence 18, Appl Sequence 19, Appl Sequence 24, Appl	, 10°, 14°, 10°, 10°, 10°, 10°, 10°, 10°, 10°, 10	1817.20	2, 2, 4,01	222 8522 561 523 520,
0-017-16 0-292-79 0-267-73 0-267-73 0-996-569	9 US-09-996-569-14 14 US-10-921-218-14 14 US-10-372-095-2 9 US-09-996-569-10 17 US-10-921-218-10 14 US-10-372-095-5	14 US-10-267-730-13 14 US-10-267-730-8 14 US-10-225-567A-1231 14 US-10-267-730-7 14 US-10-267-730-22 14 US-10-267-730-6		14 US-10-225-567A-227 15 US-10-295-027-526 15 US-10-295-027-851 16 US-10-723-860-2139 17 US-10-925-095-565 18 US-10-295-027-524 14 US-10-267-730-23 9 US-09-996-569-19
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44 4 4 4 4 4 4 4 4	0 0 0 0 0 0	44444		
113 114 116 116	18 20 20 20 20 20 20 20 20 20 20 20 20 20	4 2 2 2 2 2 2 4 2 4 2 4 5 6 6 6	1 W W W W W W W W W W W W W W W W W W W	W W W 4 4 4 4 4 4 4 7 0 0 0 0 11 01 11 11 11 11 11

ALIGNMENTS

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ULT 1 10-267-730-20 ublication US/10267730 ublication No. US20030153041A1 swized INFORMATION: SWEAL INFORMATION: APPLICANT: Seciety, Hearld APPLICANT: Dotts, Jr., John T. APPLICANT: Dotts, Jr., John T. APPLICANT: Schipani, Ernestina TITLE OF INVENTION: BARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME FILE REFERENCE: 00786/071002 CURRENT APLICATION NUMBER: US/10/267,730 CURRENT FILING DATE: 1995-06-06 FRIOR FILING DATE: 1995-06-06 FRIOR FILING DATE: 1995-06-06 EQ ID NO 20 IERGALE STEATH S91 IERGALE STEATH S91 IERGALE SPETENCE: OF WINDOWS Version 4.0 EQ ID NO 20 IERGALE SPETENCE: OF WINDOWS VERSION 4.0 EQ ID NO 20 IERGALE SPETENCE: US/10/20/20/20/20/20/20/20/20/20/20/20/20/20	Gaps	26 EVFDRLGMIYTVGYSMSLASLIVAVLILAYFRRLHCTRNYIHMIMFLSFMLRAASIFVKD
DING	6	LRAAS
ENCO	1 591 [8	LSFW
DNA	Length 591; Indela	AMEMIE
AND	DB 14; Ld	PRLHCTRNY IHMHMFLS
TOR	14	
GEP.	DB 0, hes	REL REL
3 RE	10;	AYE
494, 494	3. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	WLILAY
730 di 0/2¢ 471,	Score 410; D Pred. No. 0; 0; Mismatches	¥=¥
267 M. MBa ID JID JID JID JID JID JID JID JID JID J		ASL
S/10 041P 041P 1d 1d 1d 1d 1d 1d 1d 1d 1d 1d 1d 1d 1d	94.3%; 100.0%; ive	SMSI SMSI
O. US20030153041A1 O. US20030153041A1 MATION: egre, Gino V. Abou-Samra, Abdul-Badi Juppner, Harald Juppner, Hr., John T. Schipani, Ernestina ENITON: PARATHYROID HO CE: 00708 (07105) ICATION NUMBER: US/10/ NG DATE: 2003-01-27 ATTON NUMBER: US 08/47 DATE: 1995-06-06 Q ID NOS: 28 stSEQ for Windows Vers	94.: larity 100 Conservative	VGYSMSI
11030 11	y.	1171
US 11 CON 11 CON 11 CON 12 CON	arit	7. LG
20 No. US20030153 NRMATION: Segie, Gino V. Segie, Gino V. Kronenberg, Hara Juppner, Hara Juppner, Hara Juppner, Hara Juppner, Hara Jubpner, Ha	mil C	7.
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7-73 Constitution of the c	Matc ocal	7 2
RESULT 1 US-10-267-730-20 Sequence 20, Application US/10267730 Fublication No. US20030153041A1 GENERAL INFORMATION: APPLICANT: Segre Gino V. APPLICANT: Abou-Samza, Abdul-Badi APPLICANT: Juppner, Harry M. APPLICANT: Juppner, Harry M. APPLICANT: Schipani, Ernestina TITLE OF INVENTION: PARATHYROID HORMONE R. FILE REFERENCE: 00786/071005 CURRENT APPLICATION NUMBER: US/10/267,730 CURRENT APPLICATION NUMBER: US/10/267,730 FURRENT APPLICATION NUMBER: US/10/267,730 CURRENT FILING DATE: 1995-06-06 NUMBER OF SEQ ID NOS: 28 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 20 LENGTH: 591 TYPE: PRT ORGANISM: Rattus rattus	Query Match Best Local Similarity Matches 410; Conserv	
RESULT 1 US-10-26 Sequence Seq	Que Bes Mat	
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86 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 145
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APPLICANT: Castleberry, Tessa A.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Owen, Thomas A.
APPLICANT: Smock, Steven L.
TITHE OF INVENTION: Canine Parathyroid Hormone 1 Receptor FILE REFERENCE: PC10891AGPR
CURRENT APPLICATION NUMBER: US 609/943,446
CURRENT FILING DATE: 2001-08-30
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.1%; Score 318; DB 9; Length 591; Best Local Similarity 100.0%; Pred. No. 3.4e-292; Matches 318; Conservative 0; Mismatches 0; Indels
                                                                                     542 PATETETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQE 585
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Patent NO. US20020146777A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Oven, Thomas A.
APPLICANT: Oven, Thomas A.
APPLICANT: Smock, Steven L.
APPLICANT: Smock, Steven L.
TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor; FILE REFERENCE: PC10891AGPR
                                                                 386 PATETETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPFLLQE
                                                                                                                                                                                                         ; Sequence 8, Application US/09943446
; Patent No. US20020146777A1
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                                                                                                                                                IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY 265
                                                                                                                                                                                  362 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY 421
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  26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD 85
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APPLICANT: Castleberry, Tessa A.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Owen, Thomas A.
APPLICANT: Smock, Steven L.
TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor;
FILE REPERENCE: PC10891AGPR
CURRENT APPLICATION NUMBER: US/09/943,446
CURRENT FILING DATE: 2001-08-30
PRIOR PILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 12
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; ORGANISM: Rattus No. US20020146777Alvegicus
US-09-943-446-7
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Matches 404; Conservative
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APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Glotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01
FULE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT PILING DATE: 2003-11-26
PRIOR FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Series, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Dotts, Jr., John T.
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
FILE REPERENCE: 00706/071008
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT PILING DATE: 2003-01-27
PRIOR PILING DATE: 1995-06-06
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                                                                                                                      Length 593;
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11.3%; Score 49; DB 14; I
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                        11.3%; Score 49; DB 14; 1 100.0%; Pred. No. 2.9e-37;
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11.3%; Score 49; DB :
Best Local Similarity 100.0%; Pred. No. 2.9
Matches 49; Conservative 0; Mismatches
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 593
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10267730 Publication No. US20030153041A1 GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 1006
LENGTH: 593
LENGTH: 593
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-267-730-21
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US-10-723-860-1006
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Best Local Similarity
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APPLICANT: Liaw, Chen W
APPLICANT: Liaw, Chen W
APPLICANT: Liaw, Chen W
TITLE OF INVENTION: Protein-Coupled Receptors
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: ARRN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT PILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
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APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REPERENCE: 1920-44-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT PILING DATE: 2001-12-19
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CURRENT APPLICATION NUMBER: US/09/943,446 CURRENT FILING DATE: 2001-08-30
     PRIOR APPLICATION NUMBER: US 60/229,170
PRIOR PILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
I.ENGTH.
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APPLICANT: LifeSpan Biosciences
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PRIOR FILING DATB: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 563, Application US/09826509
Publication No. US20030204073A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
                                                                                                                                                                                                                                                                                                                                                   49; Conservative
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ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
US-09-826-509-563
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Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-225-567A-229
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LENGTH: 593
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APPLICANT: Castleberry, Tessa A.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Castleberry, Tessa A.
APPLICANT: Lu, Bihong
APPLICANT: Smock, Steven L.
TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
FILE REPERENCE: PG10891AGPR
CURRENT FILING DATE: 2001-08-30
PRIOR PILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGIN: DATE: Patentin version 3.1
SEQ ID NO 6
LENGIN: DATE: 
                                                                                                                                              Sequence 6, Application US/09943446 Patent No. US20020146777A1
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                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-10-017-161-710
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; Publication No. US20050019840A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
; APPLICANT: Lidaw, Chen W.
; APPLICANT: Lidaw, Chen W.
; APPLICANT: Lidaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G; TITLE OF INVENTION: Protein-Coupled Receptors
; TITLE OF INVENTION: Protein-Coupled Receptors
; TITLE OF INVENTION: NON-ER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR APPLICATION NUMBER: 06/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
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                                                                               121 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 169
                                                                                                                                                      277 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 325
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0; Indels
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11.3%; Score 49; DB 17; I
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0;
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Publication No. US20050118639A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION: Determination of a ligand
FILE REFERENCE: P03-0006PCT

CURRENT APPLICATION NUMBER: US/10/505,486

CURRENT FILING DATE: 2004-08-20

PRIOR FILING DATE: 2002-02-22

PRIOR FILING DATE: 2002-02-22

PRIOR FILING DATE: 2002-07-23

PRIOR FILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 233

SEQ ID NO 13
       0; Mismatches
       Conservative
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ORGANISM: Homo sapiens
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US-10-925-095-563
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       49;
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       Matches
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  Length 595;
                                               Indels
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APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR PILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 710
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100.0%; Pred. No. 2.2e-31;
ive 0; Mismatches 0;
  DB 9; Le
Query Match 11.3%; Score 49; DB Best Local Similarity 100.0%; Pred. No. 2.9 Matches 49; Conservative 0; Mismatches
                                                                                                                                                                                                                                                              Sequence 710, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 622, Application US/10292798; Publication No. US20030235833A1; GENERAL INFORMATION: APPLICANT: SUWA, MAKIKO
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Matches 43; Conservative 0;
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277 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 325

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TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME

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APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATENTIN VET: 2.1
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APPLICANT: Potts, Jr., John T.
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
FILE REFERENCE: 00786/071005
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 08/471,494
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 515
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100.0%; Pred. No. 2.2e-31;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
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Abou-Samra, Abdul-Badi
Juppner, Harald
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Schipani, Ernestina
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ASAI, KIYOSHI
                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Didelphoidea
US-10-267-730-18
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Best Local Similarity
Matches 43; Conserva
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LENGTH: 964
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### FILE REFERENCE: 00786/071005
### CURRENT APPLICATION NUMBER: US/10/267,730
### CURRENT FILING DATE: 2003-01-27
### PRIOR PILING DATE: 1995-06-06
### PRIOR FILING DATE: 1995-06-06
### NUMBER OF SEQ ID NOS: 28
### SOFTWARE: PastSEQ for Windows Version 4.0
### SOFTWARE: PastSEQ for Windows Versio
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Compugen Ltd.
GenCore version
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- protein search, using sw model OM protein Run on:

4, 2005, 06:13:35; Search time 26 Seconds (without alignments) 1609.780 Million cell updates/sec

US-09-869-565-2

435 1 MGAARIAPSLALLLCCPVLS.......RASGSARPPPLLQEGWETVM 435 score: Sequence: Title: Perfect E

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 segs, 96216763 residues Searched:

0 Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	nominal hormon		parathyroid hormon	parathyroid hormon	parathyroid hormon			secretin receptor	calcitonin recepto	~	<u> </u>	gastric inhibitory	gastric inhibitory	glucose-dependent	glucose-dependent	vasoactive intesti	vasoactive intesti	vasoactive intesti	PACAP/VIP receptor		vasoactive intesti	glucagon-like pept	glucagon-like pept	glucagon-like pept	glucagon receptor	glucagon receptor	hypothetical prote	hypothetical prote	extensin-like prot
SUMMARIES	154195	S44203	159297	A49191	A39286	A57519	JC2532	816319	A39285	147130	153273	JC2462	G02234	S66676	137411	JH0594	JC2194	JC2195	JU0185	839069	G02822	S71624	I84494	A46172	JC4363	JQ1957	S77440	T27680	T09067
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ALIGNMENTS

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		hormone
		>/parathyroid
		hormone,
1	ñ	hyroid

ated-peptide receptor - rat C,Species: Rattus norvegicus (Norway rat) C,Date: 02-Aug-1996 #sequence_revision 02

C;Date: 02-Aug-1996 #seguence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: IS4195; A42698
R;Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier 66comics 20, 20-26, 1994
A;Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor ('and rat genomes.
A;Reference number: IS4195; MUID:94292182; PMID:8020952

A,Accession: I54195 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA A,Residues: 1-591 <RES>

A,Cross-references: UNIPROT: P25961; GB:L19475; NID: 9467316; PIDN:AAA68099.1; PID: 9467317
R;Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure:
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both cAMP and inositol trisphosphates and increases intracellular free calcium.
A;Reference number: A42698; MUID:92212903; PMID:1313566

A;Accession: A42698
A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-585, G', 587-591 ABO>
A;Experimental source: ROS 17/2.8 Osteosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:92187)
C;Superfamily: glucagon receptor

Gaps ö Score 404; DB 2; Length 591; Pred. No. 0; 0; Indels 0; Mismatches 92.9%; 100.0%; 404; Conservative Query Match Best Local Similarity Matches 404; Conserval

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AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 145 85 EVPDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD 56 98 요 ò ò

242 AVLYSGFILDEABRLTEEBLHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 301 g

EGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW 205 302 146 g ⋧

265 362 IIQVPILASVVLNFILFINIIRVLATKURETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY 421 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY 206 유 ઠે

TVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLAL 325 566 422 g ò

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A;Reference number: G07787
A;Accession: G01562
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A;Status: preliminary
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C;Genetics:
A;Gene: PTHR
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385
                             DFKRKARSGSSSYSYGPWVSHTSVTWVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPGA 541
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 159297
R;McCuaig, K.A.; Clarke, J.C.; White, J.H.
R;McCuaig, K.A.; Clarke, J.C.; White, J.H.
A;Title: Molecular cloning of the gene encoding the mouse parathyroid hormor A;Reference number: 159297; MUID:94255468; PMID:8197183
A;Accession: 159297
A;Atatus: preliminary; translated from GB/EMBL/DDBJ
A;Mclecule type: DNA
A;Residues: 1-589 **RESA**
A;Residues: 1-589 **RESA**
A;Residues: 1-589 **RESA**
A;Residues: J-589 **RESA**
A;Residues: J-580 **RESA**
A;Re
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DFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPGA
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                                                                                                     PATETETLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQE
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Best Local Similarity 100.
Matches 318; Conservative
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A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 453
C;Superfamily: glucagon receptor
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A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nosidues: 1-593 ACRS.
A;Kesidues: 1-593 ACRS.
A;Cross-references: UNIPROT:003431; EMBL:U22409; NID:g897594; PIDN:AAB60657.1; PID:g89756
B;Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V
Endocrinology 132, 2157-2165, 1993
A;Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pax)
A;Reference number: A49191; MUID:93238641; PMID:8386612
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NyAlternate names: parathyroid hormone/parathyroid hormone related peptide receptor
C;Species: Home sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: 138139, #49191; 138131; 401562; 8205610
R;Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhrmann, Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
J. Cilin, Endocrinol. Metab. 80, 1611-1621, 1995
A;Title: Pseudobypoparathyroidism type Ib is not caused by mutations in the coding example of the coding experience number: 138139; MUID:95263723; PMID:7745008
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A; Residues: 1-593 «SCH»
A; Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722
A; Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722
A; Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIP:130234)
R; Schneider, H; Feyen, J.H.; Seuwen, K.; Movva, N.R.
Bur. J; Pharmacol. 246, 149-155, 1993
A; Title: Cloning and functional expression of a human parathyroid hormone receptor.
A; Reference number: 138113; MUID:93387403; PMID:8397094
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A;Molecule type: mRNA
A;Residues: 1-593 <LEV>
A;Cross-references: EMBL:U17418; NID:9596129; PIDN:AAA56774.1; PID:9596130
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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C,Accession: JC2532
R;Jiang, S.; Ulrich, C.
Biothem. Blothys. Res. Commun. 207, 883-890, 1995
A;Title: Molecular Cloning and functional expression of a human pancreatic secretin recegn A;Reference number: JC2532, MUID:95169147, PMID:7864894
A;Accession: JC2532
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT: P47872; EMBL: U20178; NID: g662795; PIDN: AAC50106.1; PID: g6627:
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A.Reseidues: 1-449 (1818-)
A.Cross-references: UNIPROT: P23811; EMBL: X59132; NID: g57228; PIDN: CAA41849.1; PID: g57229
C.Superfamily: glucagon receptor
C.Keywords: G protein-coupled receptor; transmembrane protein
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Cispecies: Sus scrofa domestica (domestic pig)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: A39285; 147129
R;Lin, H Y.; Harris, T.L.; Flannery, M.S.; Aruffo, A.; Kaji, E.H.; Gorn, A.; Kolakowski i
Science 254, 1022-1024, 1991
A;Title: Expression cloning of an adenylate cyclase-coupled calcitonin receptor.
A;Reference number: A39285; MUID:92054591; PMID:1658940
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A;Title: Molecular cloning and expression of a cDNA encoding the secretin recept A;Reference number: S16319; MUID:91266890; PMID:1646711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Rattus norvegicus (Norway rat)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C.Accession: S16319
                                                              C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.2%; Score 14; DB 2; Le
100.0%; Pred. No. 1.7e-05;
wiemmarches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:270546; OMIM:182098
A;Map position: 2q14.1-2q14.1
C;Superfamily: glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 FRELHCTRNYIHMH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRECHCIRNYIHMH 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 FRRLHCTRNYIHMH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
Les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-440 <JIA>
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A, Status: preliminary
A, Molecule type: mRNA
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A, Gene: GDB:SCTR
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A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5

A39286
parathyroid hormone / parathyroid hormone-related peptide - North American opossum
c;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Date: 24-Jan-1992
R;Jutepner, H: Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, B.; Richards, J.; Science 254, 1024-1026, 1991
A;Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel
A;Reference number: A39286; MUID:92054592; PMID:1658941
A;Status: preliminary; not compared with conceptual translation
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parathyroid hormone receptor 2 precursor - human
N;Alternate names: PTH2 receptor
C;Species: Homo sapiens (man)
N;Alternate names: PTH2 receptor
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57519
R;Usdin, T.B.; Gruber, C.; Bonner, T.I.
A;Title: Identification and functional expression of a receptor selectively recognizing
A;Reference number: A57519; MUID:95318121; PMID:7797535
A;Accession: A57519
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                                                                                                                                                                                                                                                                                      277 GYAĞCRVAVTFFLYFLATNYYMILVEĞLYLHSLIFMAFFSEKKYLMĞFT 325
                                                                                                                                                                                                                                                         121 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT
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.00.0%; Pred. No. 2.1e-09;
.ve 0; Mismatches 0; Indels
                                                                                                                               Length 593;
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A,Residues: 1-585 «JUB»
A,Cross-references: UNISOT:P25107; GB:M74445
C,Superfamily: glucagon receptor
C,Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                              0; Indels
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                                                                                                                            Query Match
11.3%; Score 49; DB 2; La
Best Local Similarity 100.0%; Pred. No. 2.6e-40;
Matches 49; Conservative 0; Mismatches 0;
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Pred. No. 2.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 NFILFINIIRVLATKLRETNAGRCDTRQQYRKLL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.8%; Score 34; DB Best Local Similarity 100.0%; Pred. No. 2.4 Matches 34; Conservative 0; Mismatches
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100.0%; Fiv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 YFLATNYYWILVEGLYLH 151
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C,Superfamily: glucagon receptor
C,Keywords: hormone receptor
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gastric inhibitory polypeptide receptor - hamster
NyAlternate names: GIP receptor
C;Species: Cricetinae gen. sp. (hamster)
C;Dape: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2462
R;Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A;Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic islets a A;Reference number: JC2462; MUID:95110292; PMID:7811236
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100.0%;
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C, Superfamily: glucagon receptor
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            159 FRRLHCTRNYIHM 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.0
Best Local Similarity 100.
Matches 13; Conservative
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les 12; Conserv
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Matches
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C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: O.2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 153273
R;Usdin, T.B.; Mezey, E.; Button, D.C.; Brownstein, M.J.; Bonner, T.I.
Endocrinology 133, 2861-2870, 1993
A;Title: Gastric inhibitory polypeptide receptor, a member of the secretin-vasoactive in A;Reference number: 153273
A;Accession: 153273
A;Accession: 153273
J. Biol. Chem. 269, 19530-19538, 1994
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcit A;Feference number: A53972; MUID:94308241; PMID:8034723
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Reference number: A53012
A;Rolecule type: DNA
A;Residues: 1-482 - 2010-
A;Cross-references: EMBL:Z31356; NID:9531126; PIDN:CAA83232.1; PID:9531127
C;Genetics:
A;Intronon: 17/3; 70/1; 144/3; 175/2; 217/3; 269/1; 289/2; 311/3; 384/3; 398/3
C;Superfamily: glucagon receptor
C;Reywords: G protein-coupled receptor; transmembrane protein
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C,Superfamily: glucagon receptor
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C, Genetics:
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C;Superfamily: glucagon receptor
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A;Molecule type: mRNA
A;Residues: 1-455 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 FQGFFVAIIYCFCN 396
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A; Cross-references: UNIPROT: P48546; EMBL: U39231; NID: 91066050; PIDN: AAA84418.1; PID: 91060
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NyAlternate names: GIP receptor
Cispecies: Homo sapiens (man)
Cispecies: Libec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
CyAccession: G02234
Ribenner, T.I.; Usdin, T.B.
Ribenner, T.I.; Usdin, T.B.
Riberner number: G09336
A;Reference number: G09336
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-466 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glucose-dependent insulinotropic protein receptor precursor - human C;Species: Homo sapiens (man) C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S66676
Gaps
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100.0%; Pred. No. 0.0018;
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A,Molecule type: mRNÅ
A;Residues: 1-466 <VOL>
A;Residues: 1-466 <VOL>
A;Cross-references: UNIPROT:P48546; GB:S79852
A;Oross-references: UNIPROT:P48546; GB:S79852
C;Superfamily: glucagon receptor
C;Superfamily: glucagon receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
P;22-466/Product: glucose-dependent insulinotropic protein receptor #status predicted <M
                             FEBS Lett. 373, 23-29, 1995
A;Title: Molecular cloning, functional expression, and signal transduction of the GIP-re
A;Reference number: S66676; MUID:96013879; PMID:7589426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: I37411
R;Gremlich, S.; Porret, A.; Hani, E.H.; Cherif, D.; Vionnet, N.; Froguel, P.; Thorens, H
B;Gremlich, 1202-1208, 1998
A;Title: Cloning, functional expression, and chromosomal localization of the human pancx
A;Reference number: 137411; MUID:96007224; PMID:7556958
A.; Goeke, R.; Lankat-Buttgereit, B.; Fehmann, H.C.; Bode, H.P.; Goeke, B.
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A;Residues: 1-491 <RES>
A;Cross-references: EMBL:X81832; NID:g1030050; PIDN:CAA57426.1; PID:g1030051
C;Superfamily: glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucose-dependent insulinotropic polypeptide receptor - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999
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Pred. No. 0.0018;
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100.0%; Pred. No. 0.0019;
tive 0; Mismatches 0; Indels
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 100.
Matches 12; Conservative
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Search completed: July 4, 2005, 06:29:04 Job time : 28 secs

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OM protein - protein search, using sw model

Run on:

July 4, 2005, 06:17:00; Search time 91 Seconds (without alignments) 2447.851 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-869-565-2 435 1 MGAARIAPSLALLLCCPVLS.......BASGSARPPPLLQEGWETVM 435

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

1612378 seqs, 512079187 residues Searched:

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

1612378

Post-processing: Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	rip	P25961 rattus norv	Q80wu8 mus musculu	Q91wv4 mus musculu	P41593 mus musculu	Q76n28 rattus norv		Q9tu31 canis famil		Q9gmd1 oryctolagus	Q8nhb4 homo sapien		P25107 didelphis m	-		_	Q9pwb7 brachydanio	Q9pvd2 brachydanio	Q91v95 mus musculu	rattu	homo	homo	рошо	homo	046502 oryctolagus		818	-	Q9rld4 mus musculu	P43219 rattus norv	_	Q802t7 fugu rubrip
SUMMARIES	ID	PTRR RAT	Q80W <u>U</u> 8	Q91WV4	PTRR MOUSE	Q76N28	PTRR_HUMAN	Q9TU31	PTRR_PIG	Q9GMD1	Q8NHB4	Q7YRI3	PTRR DIDMA		Q9PRG1	057671	Q9PWB7	Q9PVD2	PTR2 MOUSE	PTR2_RAT	PTR2_HUMAN	Q71UK6	SCRC_HUMAN	Q8IV17	SCRC_RABIT	SCRC_RAT	CALR_PIG	Q80UB4	Q9R1D4	GIPR_RAT	GIPR_MESAU	Q802 <u>T</u> 7
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٠	Query Match	92.9	78.4	1.77.7	73.1	32.4	11.3	11.3	10.6	9.9	9.9	9.5	7.8	6.4	6.2	6.0	5.7	4.1	4.1	4.1	4.1	3.4	3.5	3.5	3.2	3.5	•	٠.	3.0	3.0	3.0	7.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
                                                                                                                                                                                                                                                       Parathyroid hormone/parathyroid hormone-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
R HSSP; Q03431; 1BL1.

R RQD; 3442; PEthil.

R InterPro; 1PR010832; GPCR_secretin.

R InterPro; 1PR010832; GPCR_secretin.

R Ffam; PF020002; 7tm_2; 1.

R Pfam; PR02193; HMM; 1.

R PRINTS; PR00249; GPCRSCRETIN.

R PRNSTITS; PS00649; GPCRSCRETIN.

R PROSITE; PS00650; GPCTEIN RECEP_F2_1; 1.

R PROSITE; PS50227; GPROTEIN RECEP_F2_3; 1.

R PROSITE; PS50221; GPROTEIN RECEP_F2_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential). (Potential). (Potential).
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Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                                                Extracellular (Potential)
                                                                                                                                                                                                                                                                           related peptide receptor.
Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
By similarity.
By similarity.
N-linked (GlCNAC. ..) (EN-linked (GlCNAC. ..) (FN-linked (GlCNAC. ...) (FN-linked (GLCNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential). 2 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Preα. ...
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66260 MW;
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DOMAIN
TRANSMEM
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TRANSMEM
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DOMAIN
TRANSMEM
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SEQUENCE
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                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGD; MGI:97801; Pthr1.
GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.
GO; GO:0004891; F:parathyroid hormone receptor activity; TAS.
GO; GO:000482; P:bone mineralization; IMP.
InterPro; IPR00082; GPCR secretin.
InterPro; IPR01879; horm_receptor.
InterPro; IPR02170; Phrmn_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.4%; Score 341; DB 2; Length 591; 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051981; AAH51981.1; -.
HSSP; Q03431; 1BL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           591 AA; 66371 MW; C2E6CCAF2ABAFEEF CRC64;
                                 01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
591 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR00393; PTRHORMONER.
SMART; SM00008; HOTMR; 1.
PROSITE; PS00649; G PROTEIN RECEP F2 1; 1.
PROSITE; PS50227; G PROTEIN RECEP F2 2; 1.
PROSITE; PS50227; G PROTEIN RECEP F2 2; 1.
PROSITE; PS50261; G PROTEIN RECEP F2 3; 1.
                                                                                          Parathyroid hormone receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 341; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00002; 7tm 2; 1.
Pfam; PF02793; HRM; 1.
PRELIMINARY;
                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                Name=Pthr1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
SEQUENCE
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SEQUENCE FROM N.A. STRAIN=C3H/HEHA;
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                                                                               Receptor.
SEQUENCE
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PTRR_MOUSE
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SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE-Kidney;

STRAIN=FVB/N; TISSUE-Kidney;

STRAIN=FVB/N; TISSUE-Kidney;

STRAIN=FVB/N; TISSUE-Kidney;

STRAIN=SEGON N.A.

STRAIN=SEGON N.A.

STRAIN=SEGON N.A.

STRAIN=SEGON N.A.

SALEDHIS F.Y. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechnis R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Tobhiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Tobhiyuki S., Carninci P., Prange C.,

Rownstein M.J., Usdin T.B., Tobhiyuki S., Carninci P., Prange C.,

Brownstein M.J., Wockerna K.J., Makek J.A., Mullahy S.J.,

Boaks S.A., MocNewn P.J., McKernan K.J., Makek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

And Mones S.J., Marra M.A.,

And Mones C.J., Marra M.A.,

And Mones C.D., Shevchenko Y., Schein J.E.,

And Mones C.D., Marra M.A.,

And Mones C.D., Marra M.A.,

And Mones C.D., Schmutz J., Myers R.M., Schein J.E.,

And Mones C.D., Marra M.A.,

And Mones C.D., Schmutz D.E., Schnerch A., Schein J.E.,

And Mones C.D., Marra M.A.,

And Mones C.D., Schmutz D.E., Schnerch A., Schein J.E.,

And Mones C.D., Marra M.A.,

And Mones C.D., Schmutz D.E., Schnerch A., Schein J.E.,

And Mones C.D., Schnerch C.D., Schnerch A., Schein J.E.,

And Mones C.D., Schnerch C.D., Schnerch C.D., Schnerch C.D., Schnerch C.D., Schnerch C.D.,

And Mones C.D., Schnerch C.D.
                                                                                                                                                               265
                                                                                                         361
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                                                                                                                                                                                                                                                                            TVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLAL 325
242 AVLYSGFTLDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 301
                                                                                                                                                                                                                                                                                                                            481
                                                                               IIOVPILASVVLNFILPINIIRVLATKLRETNAGRCDTROOYRKLLRSTLVLVPLFGVHY
                                                                                                                                                                                                                                                                                                           TVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRWTLAL
                                                                                                                                                               IIOVPILASVVLNFILFINIIRVLATKLRETNAGRCDTROOYRKLLRSTLVLVPLFGVHY
                                                         EGLYLHSL1FMAFFSEKKYLWGFT1FGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0004991; F:parathyroid hormone receptor activity; TAS. GO:0030282; P:bone mineralization; IMP. GO:0001501; P:skeletal development; IMP. GO:0001501; P:skeletal development; IMP. FEME 2; 1. FEME; P:EME 2; 1.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                  DFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               DEKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRL
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PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parathyroid hormone receptor 1. Name=Pthr1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR00393; PTRHORMONER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC013446; AAH13446.1;
HSSP; Q03431; 1BL1.
MGD; MGI:97801; Pthr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (Mouse)
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                                                      146
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                                                                                                                                                                                                                                                                            566
                                                                                                                                                                                                                                                                                                                            422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91WV4
Q91WV4;
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MEDLINE=94255466; PubMed=8197183;
MCCuaig K.A., Clarke J.C., White J.H.;
MCCuaig K.A., Clarke J.C., White J.H.;
Molecular cloning of the gene encoding the mouse parathyroid
hormone/parathyroid hormone-related peptide receptor.";
Proc. Natl. Acad. Sci. U.S.A. 91:5051-5051(994).
-!- FUNCTION: This is a receptor for parathyroid hormone and for
parathyroid hormone-related peptide. The activity of this receptor
is mediated by g proteins which activate adenyly! cyclase and also
a phosphatidylinositol-calcium second messenger system.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 AVLYSGFILDEAERLTEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHY
                                                                                                                                                                                                                                                                                                                                    26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASIFVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGLYLHSLI FMAFFSEKKYLWGFTI FGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Parathyroid hormone/parathyroid hormone-related peptide receptor
precursor (PTH/PTHr receptor) (PTH/PTHrP type I receptor).
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                                                                                                                                                                                                 DB 2; Length 591;
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                                                                                                                                      66361 MW; 6E29CF63E5BAFEED CRC64;
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                                                                                                                                                                                                                                100.0%; Pred. No. 0; ive 0; Mismatches
PROSITE; PS00650; G PROTEIN RECEP F2 2; 1. PROSITE; PS50227; G PROTEIN RECEP F2 3; 1. PROSITE; PS50261; G PROTEIN RECEP F2 4; 1.
                                                                                                                                                                                                        Score 338;
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Mus musculus (Mouse).
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Matches 338; Conservative
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E SEQUENCE FORM AND AND ADDRESS OF STRAIN-Sprague-Dawley;

X XRELINE-Sprague-Dawley;

X MEDLINE-99124508; PubMed-9927318; DOI=10.1210/en.140.2.871;

RA Kawane T., Horiuchi N.;

RA Kawane T., Horiuchi N.;

RI "Insulin-like growth factor I suppresses parathyroid hormone

RT (PTH)/PTH-related protein receptor expression via a mitogen-activated

RT PROTEIN ADDRESS OF THE TABLES PARAMENT OF CONTROL OF THE CENTRY IN THE 100 CONTROL OF THE CONT
                            EGLYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKW 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Parathyroid hormone/parathyroid hormone related protein receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 AA; 15831 MW; 232775272C50B0A1 CRC64;
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PRINTS; PR00393; PTRHORMONER.
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NON TER
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                            146
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PTRR_HUMAN
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                (Potential).
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(Potential).
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2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
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Extracellular (Potential).
1 (Potential).
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F7876F8D388BDDFD CRC64;
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By similarity.
By similarity.
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Cytoplasmic (Potential).
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les 318; Conservative
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MEDLINE=99238641; PubMed=8386612; DOI=10.1210/en.132.5.2157; Schipani B., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M., Abou-Samra A.-B., Segre G.V., Jueppner H.; "Identical complementary deoxyribonucleic acids encode a human renal and bone parathyroid hormone (PTH)/PTH-related peptide receptor."; Endocrinology 132:2157-2165(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of cDNA and genomic DNA encoding the human PTH/PTHrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20374568; PubMed-10913300; DOI=10.1021/bi0001426; Grauschopf U., Lilie H., Honold K., Wozny M., Reusch D., Esswein A., Schaffer W., Rucknagel K.P., Rudolph R.; "The N-terminal fragment of human parathyroid hormone receptor 1 constitutes a hormone binding domain and reveals a distinct disulfide
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95263723; PubMed=7745008; DOI=10.1210/jc.80.5.1611; Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F., Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C., Abou-Samra A.S., Crawford J.D., Potts J.T., Jr., Kronenberg H.M., Phou-Samra A.-B., Segre G.V., Jueppner H.; Ur., Kronenberg H.M., "Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons of the human parathyroid hormone (PTH)/PTH-related
                                                                                                                                                                                                                                                                                                                 MEDLINE=93387403; PubMed=8397094; DOI=10.1016/0922-4106(93)90092-N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS JMC ARG-223 AND PRO-410.
MEDLINE=96366745; PubMed=8703170; DOI=10.1056/NEJM199609053351004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 168-198.
MEDLINE=98409426; PubMed=9737850; DOI=10.1021/bi981265h;
Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
"Binding domain of human parathyroid hormone receptor: from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95215874; PubMed=7701349; Schipani E., Kruse K., Jueppner H.; A constitutively active mutant PTH-PTHrP receptor in Jansen-type metaphyseal chandrodysplasia."; Science 268:98-100(1995).
                                                                                                                                                                                                                                                                                                                             Schneider H., Feyen J.-H., Rao Movva N.; "Cloning and functional expression of a human parathyroid hormone
                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
                                                                 receptor
                       01-0cT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
25-0CT-2004 (Rel. 45, Last annotation update)
practhyroid hormone/parathyroid hormone-related peptide r.
precursor (PTH/PTHr receptor) (PTH/PTHrP type I receptor)
Name-PTHR1; Synonyms-PTHR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Endocrinol. Metab. 80:1611-1621(1995).
 593 AA
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STANDARD;
                                                                                                       (Human)
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                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                       Homo sapiens
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HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pattern.";
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WEDLINE=21918585; PubMed=11850620; DOI=10.1038/ng844;

MEDLINE=21918585; PubMed=11850620; DOI=10.1038/ng844;

A HOPYARI S., Gokgoz M., Poon R., Geneure R.C., Yu C., Cole W.G.,

Bell R.S., Jueppner H., Andrulis I.L., Wunder J.S., Alman B.A.;

"A mutant PTH/PTHYP type I receptor in enchondromatosis.";

I. Genet. 30:306-310(2002).

-I- FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by g proteins which activate adenylyl cyclase and also a phosphatidylinositol-calcium second messenger system.

-I- SUBCELLULAR LOCATION: Integral membrane protein.

-I- TISSUB SPECIFICITY: Expressed in most tissues. Most abundant in kidney, bone and liver.

-I- DISEASE: Defects in PTHRI are the cause of Jansen's metaphyseal chondrodysplasia (MDC) [MINI-156400]. UMC is a rare autosomal dominant disorder characterized by a short-limbed dwarfism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DISEASE: Defects in PTHR1 can be a cause of enchodromatosis
DISEASE: Defects in PTHR1 can be a cause of enchodromatosis
(MIM:166000). Enchondromas are common benign cartilage tumors of
bone. They can occur as solitary lesions or as multiple lesions in
enchondromatosis (Ollier and Maffucci diseases). Clinical problems
caused by enchondromas include abkoletal deformity and the
potential for malignant change to osteosarcoma.
SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Constitutive activation of the cyclic adenosine 3',5'-monophosphate signaling pathway by parathyroid hormone (PTH)/PTH-related peptide receptors mutated at the two loci for Jansen's metaphyseal
                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION OF VARIANTS JMC ARG-223 AND PRO-410.
MEDLINE-97322091; PubMed-9178745; DOI=10.1210/me.11.7.851;
Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated with hypercalcemia and normal or low serum concentrations of the two parathyroid hormones. DISBASE: Defects in PTHR1 are the cause of chondrodysplasia Blomstrand type (BOCD) [MIM:215045]. BOCD is a severe skeletal
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MEDLINE=99415605; PubMed=10487664; DOI=10.1210/jc.84.9.3052;
Schipani E., Langman C.B., Hunzelman J., Le Merrer M., Loke K.Y.,
Dillon M.J., Silve C., Jueppner H.;
"A novel parathyroid hormone (PTH)/PTH-related peptide receptor mutation in Jansen's metaphyseal chondrodysplasia.";
J. Clin. Endocrinol. Metab. 84:3052-3057(1999).
Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
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                                                                                           parathyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98417978; PubMed=9745456; DOI=10.1210/jc.83.9.3373; Zhang P., Jobert A.-S., Couvineau A., Silve C.; "A homozygous inactivating mutation in the parathyroid
                                                                                                                                              in Jansen's metaphyseal
Schipani E., Langman C.B., Parfitt A.M.,
Kooh S.W., Colle W.G., Ubeppner H.;
"Constitutively activated receptors for
parathyroid hormone-related peptide in J
                                                                                                                                                                                            chondrodysplasia.";
N. Engl. J. Med. 335:708-714(1996).
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Mol. Endocrinol. 11:851-858(1997).
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-!- FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by 9 proteins which activate adenylyl cyclase and also a phosphatidylinositol-calcium second messenger system (By

    sumilarity!
    SUBCELLULAR LOCATION: Integral membrane protein.
    SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

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Canis familiaris (Dog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                           R GO; GO:00146020; C:membrane; IEA.

R GO; GO:0014930; F:G-protein coupled receptor activity; IEA.

R GO; GO:0004931; F:G-protein coupled receptor activity; IEA.

R GO; GO:0004931; F:parathyroid hormone receptor activity; IEA.

R GO; GO:0004931; F:parathyroid hormone receptor activity; IEA.

R InterPro; IPR001832; GPCR_secretin.

R InterPro; IPR001879; hormin_receptor.

R Fam; PF002793; HRM; 1.

R Pfam; PF002793; HRM; 1.

R Pfam; PR00004; GPCRSECRETIN.

R RINTS; RR00049; GPCRSECRETIN.

R RNSTIFS; PR00049; GPROTEIN_RECEP_F2_1; 1.

R ROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

R ROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.

R ROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTHr receptor) (PTH/PTHrP type I receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFWAFFSEKKYLWGFT 324
                                                                                                                         Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.? Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AFL67095; AAD55938.1; -- HSSP, Q03421; 1B11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                595 AA; 66308 MW; 09568ECF38D4D258 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PTHR1; Synonyms=PTHR;
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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11.3%; Score 49; DB 2; Len
11.3%; Pred. No. 1.8e-38;
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100.0%; Preα. ...
...ve 0; Mismatches
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                                                        NCBI_TaxID=9615;
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PTRR PIG
ID PTRR PIG
AC P50133;
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PROSITE; PS00649; G_PROTEIN_RECEP_F2 1; 1.
PROSITE; PS01227; G_PROTEIN_RECEP_F2 3; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2 4; 1.
3D-structure; Disease mutation; Dwarfism; G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
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related peptide receptor.
Extracellular (Potential).
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GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005834; C:integral to plasma membrane; TAS.
GO; GO:0005834; C:integral TAS.
GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.
GO; GO:0001891; F:parathyroid hormone receptor activity; TAS.
GO; GO:0001501; P:G-protein signaling, coupled to cyclic nucl.
GO; GO:0001501; P:Relectal development; TAS.
InterPro; IPR001892; GPCR_secretin.
InterPro; IPR001892; hormi_receptor.
Pfam: PF00002; 7tm __1.
Pfam: PF00002; 7tm __1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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6 (Potential).
Extracellular (Potential).
7 (Potential).
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Extracellular (Potential)
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2 (Potential).
Extracellular (Potential)
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Cytoplasmic (Potential).
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                      EMBL, U22405; AAB60657.1; JOINED.
EMBL, U22406; AAB60657.1; JOINED.
EMBL; U22407; AAB60657.1; JOINED.
EEMBL; U22408; AAB60657.1; JOINED.
EMBL; U17418; AAA56774.1; -...
PIR; I38139; A49191.
                                     AAB60657.1; JOINED.
AAB60657.1; JOINED.
AAB60657.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00249; GPCRSECRETIN.
SMART; SM00008; HOFMR; 1.
                                                                                                                                                                                PDB; 1BL1; NNR; @=168-198.
PDB; 1ET2; Model; S=168-469.
PDB; 1ET3; Model; S=168-469.
Genew; HGNC:9608; PTHR1.
                    AAB60657.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.
49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
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189
213
220
240
                                                                                                                                                                                                                                                          MIM; 168468; -. MIM; 156400; -.
                                                                                                                                                                                                                                                                                              MIM; 215045; -. MIM; 166000; -.
                                       J22403;
                                                      U22404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
SIGNAL
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TRANSMEM
DOMAIN
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TRANSMEM
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TRANSMEM
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                                                      EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9TU31
ID O9
DT O9
DT O9
DT O9
OB O9
GN NE
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Gaps

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585 AA

Length 595; Indels Euteleostomi; Sus.

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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8NHB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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Q7YRI3
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            Parathyroid hormone/parathyroid hormone-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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TISSUE-Kidney;
TGSCUB-Exidney;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288463; AAG09046.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                   PRINTS; PRO0249; GPCRSECRETIN.

PRABAT; SM00008; HormR; 1.

PROSITE; PS00649; G_PROTEIN RECEP_F2_1; 1.

PROSITE; PS0227; G_PROTEIN RECEP_F2_2; 1.

PROSITE; PS50227; G_PROTEIN RECEP_F2_3; 1.

PROSITE; PS50261; G_PROTEIN RECEP_F2_4; 1.

G-protein coupled receptor; Glycoprotein; Signal; Transmembrane. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 1; Length 585;
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nes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                              related peptide receptor.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 (Potential).
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 (Potential).

Extracellular (Potential)
7 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 (Potential).
Cytoplasmic (Potential).
By similarity.
By similarity.
N-linked (GlCNAc. . ) (P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (Potential).
Extracellular (Potential)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (Potential)
                                                                                          EMBL; U18315; AAC48619.1; -.
HSSP; Q03431; 1BL1.
InterPro; IPR000812; GPCR secretin.
InterPro; IPR01879; hormn_receptor.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF02793; HRM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTH/PTHrP type I receptor.
Name=PTHR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
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TRANSMEM
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DOMAIN
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SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.
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SEQUENCE FROM N.A.
SLWa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto Suwa M., Sato T., Okouchi H., Asai K., Akiyama Y.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB065462; BAC05721.1; -.
HSSP; Q03431; 1BL1.
HSSP; Q03431; 1BL1.
GO:0016020; C:membrane; IEA.
GO:0004930; F:G-protein coupled receptor activity; IEA.
GO:0004991; F:parathyroid hormone receptor activity; IEA.
GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
GO; GO:0004932; F:receptor activity; IEA.
InterPro; IPR000832; GPCR secretin.
InterPro; IPR001879; horm_receptor.
InterPro; IPR002170; Phrmu_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427 PYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEI 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 PYTEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 VAVTFELYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557 VAVTPFLYPLATNYYWILVEGLYLHSLIFMAFFSEKKYLMGFT 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105705 MW; 8EA72B44244DFD5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589 AA; 64017 MW; SFDF5DF8B61E72BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.9%; Score 43; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.9%; Score 43; DB 2;
100.0%; Pred. No. 2e-32;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  964 AA
                                                                                                                                                                                                                                                                        PRINTS; PR00249; GPCRSECRETIN.
PRINTS; PR00393; PTRHORMONER.
SMART; SM00008; HOTMR; 1.
PROSITE; PS00649; G PROTEIN RECEP F2 1; 1.
PROSITE; PS00650; G PROTEIN RECEP F2 2; 1.
PROSITE; PS50227; G PROTEIN RECEP F2 2; 1.
PROSITE; PS50227; G PROTEIN RECEP F2 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00393; PTRHORMONER.
PROSITE; PS00650; G PROTEIN RECEP_F2_2; 1.
PROSITE; PS50261; G PROTEIN RECEP_F2_4; 1.
                                                         G) GO:0004991; F:parathyroid hormone
G), GO:0004972; F:receptor activity; InterPro; IPR000832; GPCR_secretin.
InterPro; IPR001879; horm_receptor.
InterPro; IPR001879; horm_receptor.
InterPro; IPR002170; Phrmn_receptor.
Pfam; PF00002; TRM, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seven transmembrane helix receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00002; 7tm 2; 1.
Pfam; PF02793; HRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SEQUENCE 964 AA; 1057
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PRT;
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                                                                                                                                                                                                                                        PRINTS; PR00249; GPCRSECRETIN. SMART; SM00008; HormR; 1.
                                                                                                  EMBL; M74445; AAA30979.1; -.
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3336
3355
3376
3376
4422
4434
1114
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1145
                                                                                                                       PIR; A39286; A39286.
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585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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423
435
458
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TRANSMEM
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Matches
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Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani B.,
Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani B.,
Krolakowski L.F. Jr., Hock J., Potts J.T. Jr.,
Kronenberg H.M., Segre G.V.,
"A G protein-linked receptor for parathyroid hormone and parathyroid
hormone-related peptide.";
Science 254:1024-1026(1991).
-!-FUNCTION: This is a receptor for parathyroid hormone and for
parathyroid hormone-related peptide. The activity of this receptor
is mediated by g proteins which activate adenylyl cyclase and also
a phosphatidylinositol-calcium second messenger system.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Didelphis marsupialis virginiana (North American opossum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis.
                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
1-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Parathyroid hormone/parathyroid hormone related protein receptor.
Cervus elaphus (Red deer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTH* receptor)
Name=PTHR1; Synonyms=PTHR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                      GO; GO: 0016020; C:membrane; IEA.
GO; GO: 0016020; C:membrane; IEA.
GO; GO: 0004930; F:G-protein coupled receptor activity; IEA.
GO; GO: 0004872; F:receptor activity; IEA.
InterPro; IPR001879; horm_receptor.
Pfam; PF002002; 7tm_2; 1.
SMART; SM00008; HORMR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Liu H., Barling P.M., Ma L., Nicholson L.F.B.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY2284011, AAP93208.1;
HSSP, Q03431; 1BL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65733 MW; 08A0577FB042A77A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 KSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 KSWSRWTLALDFKRKARSGSSSYSYGPWVSHTSVTNVGPR 510
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Pred. No. 1.1e-29;
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  589 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     585 AA
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      589 AA;
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nes 40; Conserv
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                                                                                                                                                                                 Cervinae, Cervus.
                                                                                                                                                                                            NCBI_TaxID=9860;
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PTRR DIDMA
P25107;
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SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parathyroid hormone/parathyroid hormone-
related peptide receptor.

Extracellular (Potential).

Cytoplasmic (Potential).

Zytoplasmic (Potential).

Sytoplasmic (Potential).

Cytoplasmic (Potential).

Sytoplasmic (Potential).

Extracellular (Potential).

Sytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular (Potential).
7 (Potential).
Cytoplasmic (Potential).
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC. ...) (Potential).
N-linked (GlCNAC. ...) (Potential).
N-linked (GlCNAC. ...) (Potential).
N-linked (GlCNAC. ...) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00649; G. PROTEIN RECEP_F2_1; 1.
PROSITE; PS00649; G. PROTEIN RECEP_F2_2; 1.
PROSITE; PS50227; G. PROTEIN RECEP_F2_3; 1.
PROSITE; PS50261; G. PROTEIN RECEP_F2_4; 1.
G. PROTEIN RECEP_F2_4; 1.
SIGNAL 1 26
Potential : Signal; Transmembrane.
CHAIN 27 585
Parathyroid hormone/parathyroid hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99428481; PubMed=10497171; DOI=10.1074/jbc.274.40.28185;
Rubin D.A., Juppner H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%; Score 34; DB 1; Le ilarity 100.0%; Pred. No. 7.5e-24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 NFILFINIIRVLATKLRETNAGRCDTRQQYRKLL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 NFILFINIIRVLATKLRETNAGRCDTRQQYRKLL 251
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01-WAY-2000 (TrEMBLrel. 13, Last seq
01-UNA-2003 (TrEMBLrel. 24, Last ann
Parathyroid hormone receptor PTHIR.
                                                                                                                                                                                                       HSSP; Q03431; 1BL1.
InterPro; IPR000812; GPCR_secretin.
InterPro; IPR010819; hormn_receptor.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF02793; HRM; 1.
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94 AA; 10729 MW; D949182E1D2613EF CRC64;

SEQUENCE

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MEDLINE=99367425; PubMed=10438471; DOI=10.1074/jbc.274.33.23035;
Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
"A G protein-coupled receptor from zebrafish is activated by human parathyroid hormone and not by human or teleost parathyroid hormone-
related peptide. Implications for the evolutionary conservation of calcium-regulating peptide hormones ";
J. Biol. Chem. 274:23035-23042(1999).

EMBL; AR132078; AAD51906.1; BR.
EMBL; AR132078; AAD51906.1; JOINED.
REMBL; AR132078; AAD51906.1; JOINED.
ROJ GO:0016022; Cimembrane; IEA.
GO; GO:0004872; F:G-protein activity; IEA.
RIFEPPO; IRROWARD: GPCR_secretin.
express the common parathyroid hormone/parathyroid hormone-
otide receptor (PTH1R) and a novel receptor (PTH3R) that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
05-JUJ-2004 (TrEMBLrel. 13, Last sequence update)
Parathyroid hormone type-2 receptor (Fragment).
Ictalurus punctatus (Channel catfish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Siluriformes;
Ictaluridae; Ictalurus.
NCBI_TaxID=7998;
                       related peptide receptor (FFH1R) and a novel receptor (FFH3R) that preferentially activated by mammalian and fugufish parathyroid hormone-related peptide.;

I. J. Biol. Chem. 274:28186.";

E. MBL; AF132084; AAF01265.1;

R. RSP; Q03411.1BL1.

R. RSP; Q03411.1BL1.

R. GO; GO:0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004931; F:parathyroid hormone receptor activity; IEA.

GO; GO:0004931; F:receptor activity; IEA.

R. GO; GO:0004872; F:receptor activity; IEA.

R. InterPro; IPR000832; GPCR_secretin.

R. InterPro; IPR00170; Phrmn_receptor.

R. InterPro; IPR002170; Phrmn_receptor.

R. Pfam; PF00002; 7tm 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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100.0%; Pred. No. 4.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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PRINTS; PR00393; PTRHORMONER.
SMART; SM00008; HOTMR; 1.
PROSITE; PS00649; G PROTEIN RECEP F2_1; 1.
PROSITE; PS00650; G PROTEIN RECEP F2_2; 1.
PROSITE; PS50227; G PROTEIN RECEP F2_3; 1.
PROSITE; PS50221; G PROTEIN RECEP F2_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 NIIRVLATKLRETNAGRCDTRQQYRKLL 361
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Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
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Q9PRGI
DD Q9PRG
DT Q1-MA
DT Q1-MA
DT O1-MA
DT 
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016020; C:membrane; IEA.
GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000021; GFCR_secretin.
Pfam; PF00002, 7fm 2; 1.
PRINTS; PR00249; GPCRSECRETIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 26; DB 2; Length 126; 100.0%; Pred. No. 1.2e-16; tive 0; Mismatches 0; Indels
                     Length 94;
                                                                   IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Hsu C., You S., El Halawani M.E., Foster D.N.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.

NON TER 126 126
SEQÜENCE 126 AA; 14515 MW; 0F381BDB094A1A77 CRC64;
                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Parathyroid hormone receptor (Fragment).
Score 27; DB 2; Leng
Pred. No. 1e-17;
                                                                                                                                                                                                                                                                               126 AA
                   6.2%; Score 27; DB 100.0%; Pred. No. 1e-artive 0; Mismatches
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                                                                                                                134 YFLATNYYWILVEGLYLHSLIFMAFFS 160
                                                                                                                                           12 YFLATNYYWILVEGLYLHSLIFMAFFS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 LVEGLYLHSLIFMAFFSEKKYLWGFT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LVEGLYLHSLIFMAPPSEKKYLWGFT 31
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: July 4, 2005, 06:30:44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.0%;
Best Local Similarity 100.0%
Matches 26; Conservative
                     Query Match 6.29
Best Local Similarity 100.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U94326; AAB93893
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